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Ogyud oryza sativ
Ogsig occherichia
Ogsig occherichia
             Ogvarž drosophila
Ogveto drosophila
Ogveto drosophila
Ogvets americalla
Ogvets amercophaga
Oglard mus musculu
Ogtvs oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                           O96ij3 homo sapien
O9f2b7 thauera aro
O9se05 glycine max
O9hf62 ashbya goss
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Ogrvil deinococcus
  Q9w7p9 paralichthy
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01-NOV-1999 (TrEMBLrel. 1, Last sequence update)
01-NOV-2009 (TrEMBLrel. 12, Last samotation update)
F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas disease HARMOPHILLA B)) (Factor IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-88327116; PubMed-3416069;
Reitgma P.A., Bertina R.M., Ploog van Amstel J.K., Riemens A.,
Brief E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                 2222
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095nd7 pan troglod
095nd6 pan troglod
09516 ceanorhabdi
07618 ceanorhabdi
090415 tertrahymana
001136 metarhizium
0997a9 metarhizium
09442 metarhizium
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09441 metarhizium
09461 metarhizium
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Q8w236 triticum ae
28vv87 terrabacter
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Q8wzb4 homo sapien
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                                                                                                                                                                                                                                                                                                               671580
               GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Pan troglodytes (Chimpanzee).
Karayota, Metazoa, Chordas, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primetes, Getarrhini; Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparison of DNA and protein polymorphims between humans and
                                                                                                                                                             Query Match
100.04; Score 46; DB 6; Length 461;
Best Local Similarity 100.04; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0: Indala
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                                                                                                           51764 MW; 30C2F857C0F77F45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95ND6,
01-DEC-2001 (TrEMBLrel, 19, Created)
01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROGRES EXPOSIN, 1.

PROSTER PRODUCTO, ASK HYDOXYL, UNKNOWN 1.

PROSTER PRODUCTS, BGF 1; UNKNOWN 2.

PROSTER PROSTER; PROLISE; BGF 2, UNKNOWN 2.

PROSTER; PROSTER; BGF CA: UNKNOWN 2.

PROSTER; PROSTER;
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PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1. PROSITE; PS00135; TRYPSIN SER; UNKNOWN 1. Hydrolase; Serine protesses. Secons 5 et al. As, 51764 MW; 30C2P857C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geneš Genet. Syst. 0,0-0 (2001).
BMBI, AB062419; BABS8866.1;
BWBI, AB062469; BABS8866.1; JOINED.
BWBI, AB062461; BABS8866.1; JOINED.
BWBI, AB062463; BABS8886.1; JOINED.
BWBI, AB062465; BABS8886.1; JOINED.
BWBI, AB062465; BABS8886.1; JOINED.
BWBI, AB062469; BABS8886.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coagulation factor XI.
                                                                                                                                                                                                                                                                                                                                                                                376 LVDRATCLR 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimpanzees.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Satta Y.;
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Q96516
ID Q9651
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095ND6
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                                                                                                  Pan troglodytes (Chimpanzee).
Enkaryota, Netazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBL_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

100.0%; Score 46; DB 4; Length 456; Best Local Similarity 100.0%; Pred. No. 0.17; Metches 9; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 AA; 51149 MW; 54E20A1B3964E234 CRC64;
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PROSTITE, PEROGOS, REF. HYDROXYL, UNKNORN. 1.
PROSTITE, PRO1022; EGF. 1 UNKNORN. 1.
PROSTITE, PRO1167; EGF. 2, UNKNORN. 1.
PROSTITE; PRO1167; EGF. CA, UNKNORN. 1.
PROSTITE; PRO1167; GLUC CARBOXYLATION, UNKNORN. 1.
PROSTITE; PRO1167; GLUC CARBOXYLATION, UNKNORN. 1.
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IPR001881; EGF Ca.
IPR001254; Ser protease Try.
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EMBL, AB0624019. BABS8885.11 -
EMBL, AB0624016. BABS8885.11, JOINED.
EMBL, AB0624016. BABS8885.11, JOINED.
EMBL, AB062462. BABS8885.11, JOINED.
EMBL, AB062462, BABS8885.11, JOINED.
EMBL, AB062466, BABS8885.11, JOINED.
EMBL, AB062466, BABS8885.11, JOINED
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InterPro, IPR000294; Vitk_dep_GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                  Pfam; PF00008; EGF; 2
Pfam; PF00594; gla; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 LVDRATCLR 379
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SEQUENCE 456
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Q95ND7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrahymena thermophila.
Bukaryota, Alveolata; Ciliophora, Oligohymenophorea, Hymenostomatida;
Tetrahymenina; Tetrahymena.
NCBL_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Ziang H., Hang X., Berger J.D.;

"A cyclin-like sequence in Terrahymena thermophila.";

"A cyclin-like sequence in Terrahymena thermophila.";

"In SIMILARIY: BELONGS TO THE CYCLIN PAMILY.

"ISSP: P3024; UNIN.

"HSR: P3024; UNIN.

"HSR: P801014; Occlin."

"Feam P801014; Occlin."

"RemyTr SN00185; CYCLIN; 1.

"RNGTTE, P800292; CYCLIN; 1.

"RNGTTE, P800292; CYCLINS; 1.

"Ocli Cycle; Cell division; Cyclin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.3%; Score 36; DB 5; Length 909; 88.9%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 60;
                                                                                                     "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. A607754.1 A606453.11 - "LINE-PER A007754.1 A607543.11 - "LINE-PER DIPROCATOR CYS. ERNA. Synt. 1a.
PER PROLIGGERNA-Synt. 1a.
PER PROLIGGERNA-S
                                                                                                                                                                                                                                                                                                                                                                                                                            909 AA; 105316 MW; FDF4E96133864DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AA; 7020 MW; 803EC056F39D45D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAY-2001 (TrEMBLrel, 19, Last annotation update)
Mitotic cyclin-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q01136;
0.1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 5;
Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 909 AA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             811 LVDRATLLR 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LVDRATCLR 9
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                                                                                Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CU427
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001136
ID 00113
DT 01-NG
DT 01-NG
DB TYPE
GN TYRI
OS Metaa
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Q9U4L5
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Nabalidde; Peloderinae; Caenorhabditis.
NCBI TAXID6539;
                                                                                                                                                                                                                                                      Bukaryota; Metazos; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabdildae; Peloderinae; Caenorhabdilis.
NCB: TAXIDE339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating boloogy. The C. elegans Sequencing Consortium."; Science 282:2012-2018 [1998].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2;
Dempsey S., Le T.T.;
"The sequence of C. elegans cosmid Y23H5A.";
Submitted (JUL-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
Dempsey S., Le T.T.;
The sequence of C. elegans cosmid Y23H5A,";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2001) to the BMBL/GenBank/DDBJ databases.
BMSLARDYSTA1, ARKSBASE1, ...
InterPro, IRR002308, Cys. tRNA-synt_la.
Fram, PF01406; LRNA-Synt_le; 1.
ITGREAMS, ITGR00415; CysS, 1.
SEQUENCE 908 AA, 105217 WH; 0B3BC484F9772E35 CRC64;
                          01-DBC-2001 (TEMBLEE) 19, Created)
01-DBC-2001 (TEMBLEE) 19, Last sequence update)
01-JUN-2002 (TEMBLEE) 12, Last annotation update)
Hypotherical protein Y23HSA.7b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.NOV-1998 (TrEMBLrel. 08, Created)
01.NOV-1998 (TrEMBLel. 08, Last sequence update)
01.JNV-2002 (TrEMBLEL. 11, Last annotation update)
Figochetical 105.3 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                           Caenorhabditis elegans
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"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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Matches
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Screen S.B., Stleger R.J.;
"Teolation of militable procease genes from the entomopathogenic fungus
Melathizium anisoplase.";
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Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
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                                                                                                                             Gaps
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Rhizobiaceae; Rhizobium.
NCBI_TAXID-176299;
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                             Score 34; DB 3; Length 255;
Pred. No. 32;
1; Mismatches 0; Indels
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CISZ OR ATUS307 OR AGR PAT 441.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Plasmid AT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR001314; Chymotrypain.
InterPro: IPR001314; Chymotrypain.
InterPro: IPR001314; Ser_protease_Try.
InterPro: IPR001314; Ser_protease_Try.
IPR00131; SR00124; CHYMOTRYSIN.
IPR00131; SR001030; Tryp. SEr; 1.
IPR001121; PS00104; TRYPSIN IDO; 1.
IPR001172; PS001014; TRYPSIN HIS; UNRNOWN 1.
IPR001172; PS001134; TRYPSIN HIS; UNRNOWN 1.
IPR001172; PS001134; TRYPSIN HIS; UNRNOWN 1.
IPR001172; PS001134; TRYPSIN HIS; UNRNOWN 1.
IPR001173; PS001134; TRYPSIN HIS; UNRNOWN 1.
IPR001174; PS001134; PS001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypsin-related protease precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
                                   73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 12, (TrEMBLrel. 20,
                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metarhizium anisopliae.
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                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.103;
                                                                                                                                                                                                                                                                 :|||||||
173 VVDRATC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=5530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 WUDRATC 177
                                                                                                                                                                                                           1 LVDRATC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LVDRATC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (
01-NOV-1999 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ME1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Y842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y842
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merarhizium anisopliae
Bukaryosa: Pungl, Ascomycota. Pezizomycotina. Sordariomycetes;
Hyporcales: Clavicipitacese; mitosporic Clavicipitacese; Metarhizium.
KPD. Taxibes550;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium
NCBL TaxID=5530;
                                                                                                                                                                                                                                                                                         Smithson S.L., Paterson I.C., Bailey A.M., Screen S.E., Hunt B.A., CObb B.D., Cooper R.M., Charley A.K., Clarkon J.M., "Cloning and characterisation of a gene encoding a cuticle-degrading proteage from the insect pathogenic fungus Metarhizium anisopliae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 166:161-165(1995).
-!- SIMILARIYE: BEKONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submittēd (FFB-1999) to the EMEL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPEDEN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WERDES 501.101. -
TherePro 17800131.4. Chymotrypain.
InterPro 17800134. Scriptotesse_fry.
InterPro 178001254. Scriptotesse_fry.
PRINTS: PRO0722. CHYMOTRYBIN.
PROSTIE: PRO0721. TTYP. PRO.
PROSTIE: PRO0731. TTYP. PRO.
PROSTIE: PRO0134. TRYPERIN DOM.
PROSTIE: PRO0135. TRYPERIN EAS.
PROSTIE: PRO0135. TRYPERIN EAS.
PROCTEE: PRO0135. TRYPERIN EAS.
PROCTEE: PRO0135. TRYPERIN EAS.
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PROCURSE: PRO0135. TRYPERIN EAS.
PROCURSE: PRO0135. TRYPERIN EAS.
PROCURSE: PRO0135. TRYPERIN EAS.
PROCEEDING TRYPERING TRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Protease; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro. IRRODALSIA; Chymotrypain.
InterPro. IRRODALSIA; Ser_processe_Try.
Pfam; PP000089; Lrypain; 1.
SMARTS: SMOROT24; CHYMORTRYSIN.
SMART: SMOROT27; CHYMORTRYSIN.
SMART: SMOROT29; TRYPERSIN LIST.
PROSITE; PS00134; TRYPSIN LIST, UNXONN_1.
PROSITE; PS00135; TRYPSIN LIST, SRR; 1.
                                                                                                                                                                                                                                               MEDLINE=96105219; PubMed=8529882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 254 AA; 26117 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF130865; AAD29675.1; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X78875; CAA55477.1; -. HSSP; P35049; 1TRY.
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TRY2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS: S01.103: -
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Q9Y7A9
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SEQUENCE FROW N.A.
MEDLINE-21563065; PubMed=11706173;
MEDLINE-21563065; PubMed=11706173;
Delts T., Thomashow M.F.;
Components G. the Arabidopsis C-Repeat/Dehydration-Responsive Element
Binding Factor Cold-Response Pathway Are Conserved in Brassica napus
and Other Plant Species. "
Plant Physiol. 127:910-917(2001).
EMEL, AF370729; AAL35759:11.
InterPro, IROG0471; TE_RRC.
                                                                                                                                                                                                                                                                                                                                                                COUNTIES FROM N.A.
STRAINA-CTC 15592 / PAOL;
MEDLINE-COG. 15592 / PAOL;
MEDLINE-COG. 15592 / PAOL;
Stover C.K., Phan X.-O.T. Erwin A.L., Mizoguchi S.D., Marrener P.,
Stover C.K., Paum X.-O.T. Erwin A.L., Mizoguchi S.D., Marrine Hickey M.J. Brithman Y.-O. Tolentino E., Westbock-Wadman S.; Yans Y.,
Brody E.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen T.T.,
Reizer J., Salar M.H., Handcock R.E.W., Lory S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAOL, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secale cereale (Rye).
Setaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticaes; Secale.
                                                                                                                                                                                                                                             Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.7%; Score 33; DB 10; Length 212; 75.0%; Pred. No. 43; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.7%; Score 33; DB 16; Length 165; 75.0%; Pred. No. 33; 1; Indels 1; Mismatches 1; Indels
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SEQUENCE 212 AA; 23291 MW; E1D0265030102159 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE004464, AAG03650.1; -.
Hypothetical protein, Complete proteome.
Figoribust is AA, 18391 WW, C93ED41A0E251C7B CRC64,
                                         01-MAR-2001 (TrEMBLrell 16, Created)
01-MAR-2001 (TrEMBLrell 16, Last sequence update)
01-0GT-2001 (TrEMBLrell 16, Last annotation update)
Hypotherical protein PA0261.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 AA
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Probom; PD001423; TF AP2; 1.
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Best Local Similarity 75.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:959-964 (2000)
                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBF-like protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LVDRATCL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LVDRATCL 8
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=287;
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QBW599
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen Y., Pade G.E., Almedal N.F. Dr., Woo L., Chen Y., Palaen I.T., Zisen J.A., Karp D.D., Bovee D. Sr., Chapman P., Clandenning J., Deatherage G., Gillate W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenplimachak C., Wu Z., Komero P., Gordon D., Raymond C., Rouse G., Saenplimachak C., Wu Z., Komero P., Gordon D., Gordon-Kamm B., Liko L., Kim S., Hendrick C., Zheo Z.-Y., Dolan M., Knespan W., Perry M., Chunley P., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROW N.A.
MEDINE-21608515, PubMed=11743194;
MEDINE-21608515, PubMed=11743194;
MEDINE-21608515, PubMed=11743194;
MUCIOLO B., Goldman B.S., Cao Y., Abenenat M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,
Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,
Flanagan C., Crowell C., Ourson J., Lomo C., Sear C., Markelz B.,
Telanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Teledome sequence of the plant pathogen and biotechnology agent
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Bacteroides (PB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
Bacterofides.
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relamida pital and pital from Bacteroides: 5-nitroimidazole
resisteance genes and their upstream insertion sequence elements.";
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EMBL: X76949; CAASATIL1; - 2CBA79953A919FP3 CRC64;
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62.5%; Pred. No. 14;
tive 3; Mismatches 0; Indels
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EMBL; AEO07999; AAKSOBG21; ALT_INIT.
Plasmid; Complete protecme.
SEQUENCE 434 AA, 48002 MW; CSFDBDFA56B01E28 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-NOV-105C-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE=95291442; PubMed=7773395;
                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:2317-2323(2001).
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Best Local Similarity 62.55,
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RESULT 14

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K. MEDALTE-218-61062.

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*Kasuga K., Nojiti H., Yamane H., Kodama T., Omori T.,

*Choning and Characterization of genes involved in the degradation of

dibensoftwan by Terradacter ap, strain DBF63.*;

*Choning and Basenga 84.387-395(197).

*Emmit. ABOOMS63. BASE37-395(197).

*InterPro. IPRO0147, HTM Terk.

*InterPro. IPRO0147, HTM Terk.

*Pémnt, PPRO0147, Peptidase $24.

*Pémnt, PPRO0140, terk.

*Pémnt, PPRO0140, terk.

**InterPro. IPRO0140, terk.

**InterP
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Shearyota v Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooideae;
Tritoene; Triticum.
NCBI_Taxiba465;
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Bacteria, Firmidutes, Actinobacteria, Actinobacteridas,
Actinomycetales, Micrococcineae, Intrasporangiaceae, Terrabacter.
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PRINTS; PRO0726; LEXASERFTASE.
SEQUENCE 252 AA; 27167 MW; BTCSBACES9BADBA3 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
LEXA repressor-like protein.
                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative CRT/DRE-binding factor.
                                                                         212 AA.
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Q8W236;
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Q8VV87
Q8W236
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Search completed: May 6, 2003.
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Search completed: May 6, 2003, 15:02:46 Job time : 34.95 BECB

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6, 2003, 14:58:24 ; Search time 9 Seconds (without alignments) 41.476 Million cell updates/sec May Run on:

US-09-851-422B-1 46 1 LVDRATCLR 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match O% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printted, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P16293 sus scrofa	P16291 ovis aries	P16296 rattus norv	P16295 cavia porce	P00741 bos taurus	P19540 canis famil	P16294 mus musculu	P00740 homo sapien		P23984 infectious	P08922 homo sapien	P16746 human cytom	P00746 homo sapien	рошо	Q99895 homo sapien	P43433 micromonosp	P25954 bacillus su	P32942 homo sapien	P36437 chlamydomon	P98165 gallus gall	Q03001 homo sapien	_		Q64375 rattus norv	Q92791 homo sapien	P98155 homo sapien	P98156 mus musculu	P35953 oryctolagus	P98166 rattus norv	P82913 bos taurus	P37847 lycopodium	P37848 lycopodium	007972 management
. QI	FA9 PIG	FA9 SHEEP	FA9 RAT	FA9 CAVPO	FA9 BOVIN	FA9 CANFA	FA9 MOUSE	FA9 HUMAN	FA9 RABIT	VP40 ILTVT	KROS_HUMAN	ULS9 HCMVA	CFAD HUMAN	Y220 HUMAN	CLCR HUMAN	MYRB MICGR	CMGB_BACSU	ICA3 HUMAN	CHLB_CHLRE	LDVR CHICK	BPA1 HUMAN	MAUM METFL	PROB_BRUME	SC65_RAT	NOSS HUMAN	LDVR HUMAN	LDVR_MOUSE	LDVR RABIT	LDVR RAT	RT15_BOVIN		CHLB LYCCO	TRAN DINECA
Length DB	271 1	274 1	282 1	285 1	416 1	452 1	459 1	461 1	275 1	586 1	2347 1	123 1	253 1	546 1	269 1	311 1	323 1	547 1	688 1	863 1	2704 1	234 1	378 1	431 1	437 1	873 1	873 1	873 1	873 1	89 1	103 1	103 1	
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.3	78.3	73.9	711.7	711.7	71.7	9.69	9.69	9.69	on.	9.69	9.69	9.69	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4		65.2	65.2	6
Score	46	46	46	46	46	46	46	46	42	36	34	33	33	33	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	30	30	30	30
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Q64686 rattus norv	P25438 xanthomonas	007731 mycobacteri	P37824 chlamydomon	P09734 saccharomyc	P09733 saccharomyc	P04689 schizosacch	P24634 emericella	P25155 gallus gall	Q9udy6 homo sapien		P78568 agaricus bi
SI7C RAT	YI61 XANCV	CINA_MYCTU	CHLB CHLPT	TBA3 YEAST	TBA1 YEAST	TBA2 SCHPO	TBA2 EMENI	FA10_CHICK	RNF9 HUMAN	FA10 BOVIN	PUT2_AGABI
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305	346	430	444	445	447	449	451	475	482	492	546
65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2
30	30	30	30	30	30	30	30	30	30	30	30
34	35	36	37	38	39	04	41	42	43	44	45

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of 8 bioinformatics and the Emplo custaction the surpens Bioinformatics Institute of 8 bioinformatics on the use by non-profit institutions as long as its concent is in no way modified and this statement is not removed. Usage by and for commercial entitled and this statement is not removed. Usage by and for commercial entitles against equitee a litemase agreement (See http://www.isb-sib.ch/announce/or send an email to litemase agreement
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Sarkar G., Koeberl D.D., Sommar S.S.;
Sarkar G., Koeberl D.D., Sommar S.S.;
Litted sequencing of the activation peptide and the catalytic domain of the factor IX gene in stx species.";
Genomics 6:133-143(1990).
-!- FUNCTION: PACTOR IX IS A VITAMIN ** CADENDENT* PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHMAX OF BLOOD COAGULATION BY CONCERTING PACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
-!- CATALLICE. ACTIVITY: HYDIOLYSES ONE ANG-|-11e bond in factor X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PERTING AND THOS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISJUEIDE BONDS.
-i- SIMILARITY: BELONGS TO PEPTIDASE PAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FA9 RAT STANDARD; PRT; 282 AA. 01-2556; 01-2556; 01-256. 01-206-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Lest sequence update) 15-2UN-2002 (Rel. 14), Lest annocation update) 15-2UN-2002 (Rel. 14), Lest annocation update) 15-2UN-2002 (Rel. 14), Lest annocation update) 15-2UN-2004 (Rel. 14), Lest annocation update)
                               MEROSS; SOI 214; ...
InterPro. IPRO01254; SET_protease_Try.
InterPro. IPRO01254; VIKK_dep_GlA.
Pf. AR. PRO00039; VIRYSAIN, I.
PROSTITE; PRO0001; Tryp_SPG. 1.
PROSTITE; PRO0001; Tryp_SPG. 1.
PROSTITE; PRO00114; TRYPSIN DOW, I.
PROSTITE; PRO0134; TRYPSIN DOW, I.
PROSTITE; PRO0134; TRYPSIN MIS; I.
PROSTITE; PRO0135; TRYPSIN MIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46; DB 1; Length 274; 100.0%; Pred. No. 0.034;
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HSSP: P16293; 1PFX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Sarkar G., Koeberl D.D., Sommer S.S.;
Sarkar G., Koeberl D.D., Sommer S.S.;
Sarkar G., Koeberl D.D., Sommer S.S.;
Sorkar G., Koeberl D.D., Sommer S.S.;
Sorkar G., Koeberl D.D., Sommer S.S.;
Sorkar S.S.;
So
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- FOUNDATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS. HELD TOGETHER BY ORE OF MORE DISCULED BONDS.
- SIMPLEATIY: BELONGS TO PEPTIDES FAMILY SI.
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ALGU-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 14, Last sequence update)
Coagulation factor IX (EC 3.4.21.22), (Christmas factor) (Fragment)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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CHARGE RELAY SYSTEM.
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Therepro instalis; Ser protease Try.
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There is the service of t
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EMBL; X82593; CAA63337.1;
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271 AA;
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                                                                    MEROPS; S01.214;
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P16291;
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-Matches

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FA9_SHEEP RESULT 2

EMBL; M26247; AAA41162.1; -. HSSP; P16293; 1PFX.

EMBL; M26233; AAA31520.1; -.

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0; Indels

(POTENTIAL) (POTENTIAL) (POTENTIAL)

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NEDLINE=82272386; PubMed=6287289;
Choc X.H., Gould K.G., Rees D.J.G., Brownlee G.G.;
*Molecular cloning of the gene for human anti-haemophilic factor IX.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katayama K., Ericsson L.H., Enfield D.L., Walsh K.A., Neurath H., Davie B.W., Titani K., "Comparison of and caid sequence of bovine coagulation Factor IX (Christmas Pactor) with that of other vitamin K-dependent plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
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InterPro, IRR001254, Ser_protease_Try.
InterPro: IRR00294, VIK_dep_GLA.
InterPro: IRR00294, VIK_dep_GLA.
SWART; SM00204, TryP_Str, 1.
SWART; SM00204, TryP_Str, 1.
SWART; PS0011, GLÜ GARBOXLANION, PARTIAL.
PROSTITE, PS00114, TRYPSIN MIS; 1.
PROSTITE, PS00115, TRYPSIN MIS; 1.
BROGTER, PS00115, TRYPSIN MIS; 1.
BROGTER, PS00115, TRYPSIN MIS; 1.
BROGTER, PS00115, TRYPSIN SER; 1.
SWICH, TRYPSIN SER; 1.
SWICH, TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 46; DB 1; Length 285; 100.0%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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17-JUN-2002 (Rel. 41, Last annotation update)
Cosgulation factor IX (EC 3.4.21.22) (Christmas factor).
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Proc. Natl. Acad. Sci. U.S.A. 76:4990-4994(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-dependent blood coagulation zymogens.";
Biochem. Biophys. Res. Commun. 115:8-14(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches.
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine)
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21-JUL-1986 (
15-JUN-2002 (
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P00741,
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MEDUTES-015267; bubMed=21013254;

SEARAR G., Koeberl D.D., Sommer S.S.;

"Direct sequencing of the activation peptide and the catalytic domain of the factor IX gene in six species.";
Genomics 6.133-143(1990).
-! FOWCTION: FARTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPARES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING PACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND PACTOR VIIIA.
-! CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-11e bond in factor X to
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ng as its content is in no
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-- SUBBUNIT: REFORD IX IS ACTIVATED BY PACTOR XIA, WHICH EXCISES THE ACTIVATION PERTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OF WORRE DISELEDE BONDS.
-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AVG-1990 (Rel. 15, Last sequence update)
L-UN-2002 (Rel. 14), Last annocation update)
Cosquilerion factor 1X (EC 3.4.2.1.22) (Christmas factor) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinaa pig).
Bukaryota, Metazos: Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalis, Butheria, Rodentia, Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                        SWART, SW00020, Tryp SPC 1.
PROSITE, PSU0011, GLÜ CKABOXIVATION, PARTIAL.
PROSITE, PSU0011, GLÜ CKABOXIVATION, PARTIAL.
PROSITE, PSU0134; TRYPSIN BIS, 1.
PROSITE, PSU0135; TRYPSIN BIS, 1.
PROSITE, PSU0135; TRYPSIN SER, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 46; DB 1; Length 282; 100.0%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31447 MW; 88B37B0A4673BEC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
N-LINKED (GLCNAC. .)
                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                          InterPro, IPR001254; Ser protease_Try.
InterPro, IPR000294; VitK_dep_GLA.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                             Hydrolase; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 LVDRATCLR 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=10141;
      MEROPS; S01.214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (
01-AUG-1990 (
15-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FA9 CAVPO
P16295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Gaps

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us-09-851-422b-1.rsp

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Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.,
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                                                                                                                                     (POTENTIAL)
                            PACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
ACTIVATION PEPTIDE
RACYOR IXA (ACTIVE FORM) HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIA
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Last sequence update)
2-UN-2002 (Rel. 41, Last amocation update)
Cosquilation factor 1X precursor (EC 3.4.21.22) (Christmas factor)
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Wakaryota; Metazoa, Chordata; Craniata; Vercebrata; Euteleostomi;
Rammālia; Euthbria; Carrivora; Pissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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GAMMA-CARBOXTGUTMAIL ACID
GAMMA-CARBOXTGUTMAIL ACID
GAMMA-CARBOXTGUTMAIL ACID
GAMMA-CARBOXTGUTMAIL ACID
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GAMMA-CARBOXTGUTMAIC
GAMMA-CARBOXTGUTMAIC
BY SIMILARITY

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N-LINKED (GLCNAC. ).
CHARGE RELAY SYSTEM.
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CLEAVAGE (BY FACTOR XIA)
EGF-like domain
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Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990)
                                                                                                                                                                                                        SERINE PROTEASE
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MEDLINE=90311364; PubMed=2367529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.04;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog)
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270
366 ·
64
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P19540;
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                                                              STRUCTURE OF CARBOHYDRATE ON SER-53.
MEDINES-3144109; DubMed-2129367;
Wannaga S., Winfinura H., Kawabata S., Kielel W., Hase S., Ikenaka T.;
"A new tilsaccharide sugar chain linked to a serine residue in the
first EGF-like domain of clotting factors VII and IX and protein Z.";
4dy. EXP. Med. BIOJ. 28:1121-131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 265:1858-1861 (1990).

- FUNCTION: PACTOR IX TAS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICICAMINES IN THE INTRINCIC PATHANY OF BLOOD COAGULATION BY CONVERTING PACTOR X TO TITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND PACTOR VIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - I- SUBJUILT: PACTOR IX S.

- SUBJUILT: PACTOR IX IS ACTIVATED BY PACTOR XIA, WHICH EXCISES THE ACTIVATION PERTINE AND THIS PRODUCES A MOLECULE CONSISTING OF 2.

- HIGGELANDROS CALCIUM BINDS TO THE GAMMA-CARBOXYGLITAMIC ACID (GLA) RESIDUES AND WITH STRONGER APPINITY, TO ANOTHER SITE, BEYOND THE GLAD DOMAIN HIS CIPAL DOMAIN SEDUCES PAWILY.
                                                                                                                                                                                                                                                                                                                               MEDLINESO0130422; PUNMed=2105311.
MEDLINESO0130422; PUNMed=2105311.
"The Structure of (xylose) Zglucose-O-serine 53 found in the first withe structure of (xylose) Zglucose-O-serine 53 found in the first XX."; X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterProj : IPR001254; Ser processe Try .
InterPro; IPR000294; VitK dep GLA.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                                                                                                                                 STRUCTURE OF CARBOHYDRATE ON SER-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR002383; GLA blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
J. Biochem. 104:867-868(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00007; AAA30520.1; -.
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HSSP; P00740; 1CFH.
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CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY) CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY)
                 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Madaryota, Metazoa, Chordata, Czaniata, Vertebrata; Euteleostomi;
Bamaalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinas, Mus.
FACTOR IXA (ACTIVE FORM) HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 17, Last sequence update)
(Rel. 41, Last unctation update)
(Rel. 41, Last unctation (EC 3.4.21.22) (Christmas factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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BY SIMILARITY.
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CAMMA-CARBOXYGUTAMIC ACID

(BY SIMILARITY)

CANENA CARBOXYGUTAMIC ACID

GANNA CARBOXYGUTAMIC ACID

GANNA CARBOXYGUTAMIC ACID

(BY SIMILARITY)

(BY SIMILARITY)
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
G -> B (IN HEMOPHILA B).
W, 1P6537C46A6960ED CRC64;
                                                                                           GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY). GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                     GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                           (BY SIMILARITY).
                                                 SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                          (BY SIMILARITY)
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(Rel. 17, Last seq.
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SEQUENCE FROM N.A.
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P16294;
01-AUG-1990 (
01-FEB-1991 (
15-JUN-2002 (
Coagulation E
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F9 OR CF9.
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VARIANT
SEQUENCE
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                                                 DOMAIN
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                                                               SITE
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                                                                                                                                                                                    PRINCTION: PECTOR IX IS A VITAMIN K-DEPRINDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHMAX OF BLOOD COAGLATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS: PROSPROJEDIDS AND PACTOR WILLIA.

FORMALTIC ACTIVITY: HYDIOJAYSES ONE ARSI-1-ILE BOND IN FACTOR TO
                                                                                                                                                                                                                                                                FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
ACTIVATION PEPTIDE.
                                                                                                          MEDLINE-9009303; Pubwed-2481310; Sasans J. P., Brithous K.M., Farans J. P., Brithous K.M., Brayer G.D., Reisner H.M., High K.A.; "Canine hemophilia B resulting from a point mutation with unusual
                              Evans J.P., Watzke H.H., Ware J.L., Stafford D.W., High K.A., Wolchular cloning of a cDNA encoding canine factor IX."; Biood 7g. 1207-212(1989).
                                                                                                                                                        consequences.";
Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMOURS, SAL ZAA,
INERPEPO, IRRODIAI, ARX hydroxyl.
INERPEPO, IRRODIAI, Chymorrypin.
INERPEPO, IRRODIAI, CHymorrypin.
INERPEPO, IRRODIAI, EGF Ca.
INERPEPO, IRRODIAI, EGF Ca.
INERPEPO, IRRODIAI, EGF CA.
INERPEPO, IRRODIAIS
  TISSUE=Liver;
MBDLINE=89323338; PubMed=2752110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M21757; AAA75006.1; -. EMBL; M33826; AAA30844.1; -. PIR; A30351; A30351. HSSP; P00740; 1CFH.
                                                                                           VARIANT HEMOPHILIA B GLU-418
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Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
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Gaps

MEDLINE=90215309; PubMed=2323576;

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MEDLINE-86000558; PubMed-2994716;
Yoshitake S., Scheadn B.G., Foster D.C., Davie E.W., Kurachi K.,
"Nucleotide sequence of the gene for human factor IX (antihemophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (Rel. 06, Last sequence update)
2-JUN-2002 (Rel. 14), Least annocation update)
Coagulation factor 1X precursor (RC 3.4.71.22) (Christmas factor)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-85190953 Pobbed-3857619,
MGGENR-RA., DEVIE L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
SIMILARITY.
BY SIMILARITY.
CHARGE GGLORG. . . ) (POTEWIT
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                                                                                SAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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-> I (IN REF. 2)
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01-JAN-1988
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P00740;
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FA9 HUMAN
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                                                                                                                                  SEQUENCE OF 168-451 FROM N.A.

SERVINES OF 168-451 FROM N.A.

SERVINES-90152675; Pubbled-231347;

SERVINES-90152675; Pubbled-231347;

SERVINES-90152675; Pubbled-231347;

SERVINES-17 Gene In SIX SERVINES OF SERV
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CLEAVAGE (BY PACTOR XIA) (BY SIMILARITY)
GARMA-CREOXYGLOTAMIC ACID
(BY SIMILARITY)
Wu S.-M., Stafford D.W., Mare J.,
"Deduced maino acid sequence of mouse blood-coagulation factor IX.",
gene 864275-278(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form factor Xa.

- SUBGNIT: PROTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PERPINE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOCETHER BY ORD OR MORE DISILETIDE BONDS.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
- SIMILARITY: CONTAINS 2 EGF-LIKE DOMNINS.
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Mydrolase; Olycoprotein: Vitamin K; Gamma-carboxyghutamic acid;
Hemophilia: Hydroxylation; Zymogen; Signal; BGP-like domain;
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PROSITE, PRODILI, GGF CA, 1.

PROSITE, PRODOLI, GLU CARBOXYLATION, 1.

PROSITE, PROSIDE, TRYPELN DOM, 1.

PROSITE, PRODILS, TRYPELN HIS, 1.

PROSITE, PSODILS, TRYPELN JESS, 1.
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Interpro; IPR001742; BGF 2.
Interpro; IPR001254; BGF 2.
Interpro; IPR001254; BGF DEVCERO TY.
Interpro; IPR000294; VitK_dep_GLA.
FEam, PP00009; ETYP9in; 1.
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SNART: SMORD19; EDE CA: 1.

SNART: SMORD09; GLA-1.

SNART: SMORD000; TRYD SPC: 1.

PROSITE; PRODOSTO SECTION SECTIO
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EGF-like.
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EMBL; M26236; AAA37630.1; -.
PIR; JQ0419; JQ0419.
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MGD, MGI:88384; F9
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                                                                                         SIGNAL SEQUENCE CLEAVAGE SITE
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MEDLINE=83308813; PubMed=6688526;
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MEDLINE=97199336; PubMed=9047312;

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15-JWN-2002 (Rel]. 41 Lest annotation update)
Capsid protein P40 (Contains: Capsid protein VP24 (Assemblin)
[Feccesse] (EC 34.2.77); Capsid protein VP2A].
[Feccesse] (EC 34.2.77); Capsid protein VP2A].
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Alphaherpesvirinae; bird herpesviruses;
Infectious laryngotrachetis-like viruses.
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MEDLINE=90218031; PubMed=2157797;
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MEDLINE=90301509; PubMed=2163526;
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"Refilement of the NNR solution erructure of the
"sman-teathoryglutemic acid domain of coagulation factor IX using
molecular dynamics simulation with initial Ca2+ positions determined
Biochemistry 36:2132-2188(1997).
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-! SUBGNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR WORR DISSULPIDE BONDS.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
    Freedman S.J., Furie B.C., Furie B., Baleja J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95130802; Pubweda-760579;
Rato Z., Handford P., Neyhaw M., Knott V., Brownlee G.G., Stuart D.;
The structure of a Ca(2+)-binding epidermal growth factor-like
domain: Ite role an protein-protein interactions.";
Gell 82.111-141(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                            growth
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Coagulation factor IX (EC 3.4.21.22) (Christmas factor) (Fragment).
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Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93284090; PubMed=1304885;
Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
Tee A.G.D., Brownlee G.G., Campbell I.D.C.;
"The Libres-dimensional structure of the first EGF-like module of
                                                                                                                                                                                                                                                                                                                                                       Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V., vsequence-specific II with a secondary structure, and location of the calcium binding site in the first epidermal grow factor like domain of blood coagulation factor IX., sistopenenistry 30:7402-7409(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human factor IX: comparison with BGF and TGF-alpha.";
Protein Sci. 1:81-90(1992).
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Last annotation update)
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01-AUG-1990 (Rel. 15, Last sequ
15-JUN-2002 (Rel. 41, Last anno
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P16292;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as the order is in no way modified and this statement is not removed. Usage by and this statement is no reprofite and this statement is no removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license&isb-sib.ch/.
                                                                                                                            tyrosine phosphate.
--- SURGELULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELOAGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
RECEPTOR SUBPAMILY.
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"Characterization of an activated human ros gene.", Mol. Cell. Biol. 6:1099-116 (1989-11) of the committee o
                                                                                                                    -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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SMART; SMOODO; RNJ;
SMART; SMOODO; RNJ;
SMART; SMOODO; RNJ;
RNC1; SMOODO; PROFIEIN KINASE_ARP; 1.

PROSITE; PRO10; PROFIEIN KINASE_TRE; 1.

PROSITE; PRO10; PROFIEIN KINASE_TRE; 1.

PROSITE; PRO10; PROFIEIN KINASE_DM; 1.

TRAINER; PROSITE; PROFIEIN KINASE_DM; 1.
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ATP (BY SIMILARITY).
PHOSPHORYLATION (AUTO-)
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PROTEIN KINASE.
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Interero, 1PR000719; Buk_pkinase.
Interero, 1PR001961; PW III.
Interero, 1PR001031; Ldl receptor rep.
Interero; 1PR001031; Ldl receptor rep.
InterPro; 1PR001245; Tyr_pkinase.
Pfam; PR00041; fn3; 7.
Pfam; PR00069; pkinase.
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EMBL; M13593; AAA60277.1;
EMBL; M13594; AAA60277.1;
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EMBL; M13596; AAA60277.1;
EMBL; M13597; AAA60277.1;
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EMBL; M13880; AAA36580.1;
PIR; A25223; TVHURS.
PIR; A2421; TVHURT.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outeration the Burgapan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license&alsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                 Dr. 1859; Parts.

A EMBL, D00556; BAAL.

B PIR, S1444; S1144.

B RISSP, Parts.

DR HASSP, Parts.

PT CHAIN 240 7558 COAT PROTEIN W224 (PROTEASE).

FT CHAIN 240 7558 COAT PROTEIN W224.

FT CHAIN 
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15-UN-2002 (Rel. 41, Last annotation update)
Proto-oncogene tyrosine-protein Kinase ROS precursor (EC 2.7.1.112)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                TERMINUS (BY SIMILARITY).
CATALYTIC ACTIVITY: Cleaves -Ala-|-Ser- and -Ala-|-Ala-bonds
        WHICH CAN PROTEOLYTICALLY CLEAVE ITSELF AND VP22A AT THE C-
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BLINES-87066425; Pubmded=378523;
BLYChmeis-C., Elirnbaum D., Waltches G., Fasano O., Wigler M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsushime H., Wang L.-H., Shibuya M.;
"Human c-ros-! gent homologous to the v-ros sequence of URZ
vitus encodes for a transmembrane receptorlike molecule.";
Mol. Cell. Biol. 6:3000-3004 (1985).
                                                                                    the scaffold protein
--- SIMILARITY: BELONGS TO PEPTIDASE PAMILY 21.
--- SIMILARITY: TO OTHER HERDESVINGSE CAPSID PROTEIN VP40.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 4), Last annotation update)
Complement factor D prequency (EC 34.21.46) (G3 convertase activator)
(Properdin factor D) (Adipsin).
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson D.M.A., Gagnon J., Reid K.B.M.;
*Mailo acid sequence of human factor D of the complement system.
$\text{Similarity} in sequence between factor D and processes of non-plasma
$\text{Similarity} in sequence between factor D and processes of non-plasma
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VOlanakis U.E., Bhown A.S., Bennett J.C., Mole J.E.;
"Petrial amino acid sequence of human factor D:homology with serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAKTIAL SEQUENCE OF 26-61 AND 194-220.

WEDITRE-84256515; PUNMOGE081172;
JOHNSON D.M.A., Gegnon J., Reid K.B.M.;
PRACTOR DO I the alternative pathway of human complement.
PRACTOR DO A THE Alternative pathway of human complement.
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PRACTOR DO A THE ALTERNATIVE PATHWAY OF HUMAN COMPLEMENT.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=8500441; PubMede6383466;
MEDRINE=8500441; PubMed 8.5. Pennett J.C., Volanakis J.E.;
*Amino acid sequence of human D of the alternative complement
Indele
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HEDLINE-8105486; PubMed-6776531;
DAVIB A.E. III;
"Active site amino acid sequence of human factor D.";
Proc. Natl. Acad Sci. U.S.A. 77.4938-4942[1980).
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Proc. Natl. Acad. Sci. U.S.A. 77:1116-1119(1980)
                                                                                                                                                               253 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flier J.S., Spiegelman B.M., Rosen B.M.,
Patent number W09006365, 14-JUN-1990.
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MEDLINE=94118317; Pubmed=8289289;
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MEDLINE=84108950; PubMed=6363133;
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15-DEC-1998 (Rel. 37, Last seq
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6; Conservative
                                                                                                                                                               STANDARD;
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                                                         3 LVDQESCLR 11
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P00746;
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Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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Pred. No. 6.8;
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Viruses; dsDNA viruses. no RNA Berge: Herpesviridae;
Bvianberpesvirinae; Cytomegalovirus.
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QC -> KS (IN REF
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01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Hypothetical protein UL59.
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Matches 7, Conservative
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Hypothetical protein.
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P16746;
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Length 253; 1; Indels

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Loftus B.J., Kim U. J., Smeddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deallactes Mays A., Gao Y., Xu R.X., Kang H.-E., Mitchell S.,
Brilattes Mays A., Gao Y., Xu R.X., Kang H.-E., Mitchell S.,
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome (fog and leg.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISGUE-Bone marrow, MEDINE-STIESTE-BONE MARTON TO THE MEDINE-STIESTE-SAIN N. ISHIKAWA K.-I., Ohira M., Kawarabayasi Y., Nagase T., Seki N., ISHIKAWA K.-I., Ohira M., Kawarabayasi Y., Nagase T., Saki N., ISHIKAWA K.-I., Ohira M., Momira M., "Nomira M." Nomira M." Nomira M." Nomira M." Nomira M." Nomira M." Nomira M." The coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of CDNA clones from cell line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Makaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 546 AA; 60996 MW; F09D0824566CEF71 CRC64;
      S -> T (IN REF. 3).
S -> H (IN REF. 3).
MISSING (IN REF. 4).
; BD553B70BD55C6AD CRC64;
                                                                             ; Score 33; DB 1;
; Pred. No. 14;
. 2; Mismatches
                                                                                                                                                                                                                                                                        16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
16-00T-2001 (Rel. 40, Last sequence update)
18-00T-2001 (Rel. 40, Last shortetion update)
KIAA0220.
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EMBL; AC003007; AAC31670.1;
      243 S
250 S
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66.7%;
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Matches 6; Conservative
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                                                 253 AA;
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Q92617; 043332;
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute: There are no restrictions on its use by non-profit institutions as long as its content. Is in no way modified and this statement is not removed. Bagge by and for commercial entities a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensee@stab.sib.ch/.
Marayana S.V.L., Carson M., El-Kabbani O., Kilpatrick J.M., Moore D.,
Chen X., Bugg C.S., Volamarks J.E., Delucas L.J.;
Cstructure of human datorto D. A complement system protein at 2.0-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interprofit Depoil 114; Chymotrypsin.
Interprofit PR001294; Ser_protease_Try.
Pfan; PR001294; Ser_protease_Try.
Pfan; PR001295; Ser_protease_Try.
Pfan; Sen0030; Trypain.
SAMAT; SE00304; Trypain.
SAMAT; SE00304; Trypain.
PROSITE; PS00134; TRYPEN USH; 115; 1
PROSITE; PS00135; TRYPEN USH; 115; 1
Complement alternate pathway; Plasma; Hydrolase; Serine protease; Zimogen; Glycoprotein, Signal; Josetructure.
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M -> P (IN RRF 6).

M -> P (IN RRF 6).

G -> P (IN RRF 1 AND 5).

S -> T (IN RRF 1).

HSLS -> THLP (IN RRF 3).

HSSNG (IN RRF 4).
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                                                              Mol. Biol. 235:695-708(1994).
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Genew; HGNC:2771; DF.
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PDB; 1DST; 11-JUL-96.
PDB; 1DSU; 17-AUG-96.
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Gaps

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268 AA.

PRT;

STANDARD;

CURRTHHDGAITE -> KCRLYDVL (IN REF. 4).

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S -> T (IN REF. 1).
N -> D (IN REF. 3).
460BF33B4A96516F CRC64;
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29484 MW;
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les 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Caldecrin is a novel-type serine procease expressed in pancreas, but its howaging, elseates 1V, is an artifact during cloning derived from caldecrin gene : ; [Expm caldecrin is is caldecrive; is calde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-paracress; PubMed=8615596; MILLINE-96221265; PubMed=8615596; PubMed=8615596; PubMed=8615596; PubMed=86187; PubMed=86187; PubMed=86187; PubMed=86187; PubMed=86187 closhing and expression of human caldecrin."; PERS Lett. 186:26-28(1996).
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-- CANALYIX ACTIVITY: Preferential cleavage: Leu- |-Xaa, Tyr-|-Xaa, Phe-|-Xaa, Tyr-|-Xaa, Tphe-|-Xaa, Tphe-|-Xaa, Tphe-|-Xaa, Tphe-|-Xaa, Thel-Xaa, Asn-|-Xaa, Thel-Xaa, Tissus SPECIFITY: PANGRAS.
-- SIMILARITY: BELONGS TO PEPTIDASE PAMILY SI. ELASTASE SUBFAMILY.
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Yoshino-Yasuda I., Kobayashi K., Akiyama M., Itoh H., Tomomura A.,
                                                                                                                                                                                                                                                                                                         Bukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A human pancreatic chymotrypsin: biochemical and molecular claracterization." (Characterization.") to the EMBL/GenBank/DDBJ databases. Submitted (JUN-1997) to the
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                                          18-0cr_2001 (Rel. 40 Created)
18-0cr_2001 (Rel. 40, Last sequence update)
18-0cr_2001 (Rel. 40, Last amoration update)
06aldecrin precursor (RC 3.4.21.2) (Chymotrypein C)
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein 🗣 protein search, using sw model

Run on:

May 6, 2003, 14:59:05 ; Search time 15:75 Seconds (without alignment) (without cell updates/sec 54:934 Million cell updates/sec

US-09-851-422B-1 Title: Perfect score: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 LVDRATCLR 9

Sequence:

283224 Total number of hits satisfying chosen parameters: 283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

STIMMARTES

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ALIGNMENTS

RESULT 1 146580

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		Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999				Title: Direct sequencing of the activation peptide and the catalytic domain							Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsi:
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ctor IX - pig (iragment)	Species: Sus scrofa domestica (domestic pig)	-F	Accession: 146580	Sarkar, G.; Koeberl, D.D.; Sommer, S.S.	nomics 6, 133-143, 1990	ire	Reference number: 146580; MUID: 90152675; PMID: 2303254	Accession: 146580	Status: preliminary; translated from GB/EMBL/DDBJ	Molecule type: mRNA	Residues: 1-271 <sar></sar>	Cross-references: GB:M26235; NID:g164450; PIDN:AAA31031.1; PID:g164451	ij
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n homology 7,45-271/Domain: trypsin homology (fragment) <TRY>

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194 LVDRATCLR 202

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cosquiation factor IXa (EC 3.4.21.22) - sheep (fragment)
(Species Ovis orientals arises, Ovis amon arises (domestic sheep)
(Species 16-Oct-1968 #sequence_revision 15-Oct-1996 #text_change 22-Uun-1999
(SAccession: 147078
Risarkar, G.; Rocherl, D.D.; Sommer, S.S.

Capacitics (2, 13-143, 13-199)
A.Title. Direct eaquencing of the activation peptide and the catalytic domain of the far.
A.Recession under: 146580, MUID:90152675; PMID:2303254
A.Recession: HAPPO and A.R.
A.Recession: Trype and A.R.
A.Residues preliminary: translated from GB/EMBL/DDBJ
A.Residues preliminary: translated from GB/EMBL/DDBJ
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A.Residues 1.274 - 63RA
A.Residues 1.274 - 63RA
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Query Match 100.0%; Score 46; DB 2; Length 274; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels 1 LVDRATCLR 9 ઠ

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R.WcWullen, B.A.; Pujikawa, K.; Kisiel, M. Biglichen Biophys. Res. Commun. 115. 8-14, 1983 Bicchen Biophys. Res. Commun. 115. 8-14, 1983 A.; Fitle: The occurrence of beet-hydroxyapartic acid in the vitamin K-dependent blood or A; Fitle: The occurrence of beet-hydroxyapartic acid in the vitamin K-dependent blood or A; Faceferone umber: A20274; MUID:83308813; PMID:8689826
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A;Crediders 22-139 -CHD.
A;Crose-references 163.70007; NID:g163053; PIDN:AAA30520.1; PID:g163054
A;Crose-references 163.70007; NIBHAmura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Biochem. 104, 867-868, 1988
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa.
A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa.
A;Contentes annotating
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Comment: Estock XI & activated by factor XIA, which excises the activation peptide pr
C;Comment: The gamma-carboxyglutanic acid residues arise by posttranslational, vitemin B
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. Description: catalyzes the proteolytic activation of coagulation factor X in the pres A. Pescription: catalyzes the proteolytic activation of coagulation factor X; EGF homology of CR-words: before coagulation factor X; EGF homology of CR-words: beta Pydroyagartic acid, blood coagulation; calcium binding; carboxygluta F.1.146/Product: coagulation factor IXa 119th chain #status experimental -ALC> F.1.45/Domain: EGF homology (Eragment) -GLA> F.1.46/Product: coagulation factor IXa 119th chain #status experimental -ALC> F.18-18/Domain: EGF homology EG2> F.14-18/Domain: EGF homology EG2> F.14-18/Domain: EGF homology EG2> F.14-18/Domain: EGF homology Ed2> F.14-18/Domain: EG1-18/Domain: EG1-18/EG1-18/Domain: EG1-18/EG1-18/EG1-18/EG1-18/EG1-18/EG1-18/EG1-18/
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A.Residues: 1-452 -2014.
A.Residues: 1-452 -2014.
A.Cross-references: GB.M31757; MID.9972719, PIDN:AAA75006.1; PID:9163948
A.Cross-references: GB.M31757; MID.9972719, Vorme, 1.M.
Proc. MRLI, Acad. GB.C. U.S.A. 677 1579-1579, 1990
Proc. A.Fille: Phenorypic correction of factor IX deficiency in skin fibroblasts of hemophilic.
A.Reference number: 146201; MID:90311364; PMID:3367529
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A;Readdues: 59-63, Y. 55-59 cMCM>
R;Choo; K.H.; Yould, K.G.; Rees, D.J.G.; Brownlee, G.G.
Nature 29, 178-180, 1982
A;Title: Wolecular clouning of the gene for human anti-haemophilic factor IX.
A;Reference number: 145891, MUID:82272386; PMID:6287289
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C.Species. Canis lugas familiaris (dog).
C.Dase: 10-06p.1999 #sequence_revision 10-8ep.1999 #text_change 10-8ep.1999
R.Dase: 10-06p.1999 #sequence_revision 10-8ep.1999 #text_change 10-8ep.1999
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Matches 9; Conserv
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A; Status: preliminary
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C.Species. Bon pringhtles reuture (catla)
C.Species. Bon pringhtles reuture (catla)
C.Species. Bon pringhtles reuture (catla)
C.Species. Bon pringhtles reution 01-Aug-1984 #text_change 16-Jul-1999
C.Accession. A.4777; BD0274; T.Species. A.0023;
R.Kateayam. A.4777; BD0274; T.Species. D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti
R.Kateayam. A.602; C.S.; U.S.A.76; 4930-4994; D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti
A.7tite: Comparison of manno and sequence of boyine coagulation factor IX (Christmas fa
A.Accession: A4475; WUID:80056619; PMID:291916
                                                                                                                                                                                                                                                                                            C.Accession: 148144
Ribarkar, C.A. Koeberl, D.D.; Sommer, S.S.
Ribarkar, G. 133-143, 1990
A.Title: Direct sequencing of the activation peptide and the catalytic domain of the fac
A.Reference number: 146580; MUID:90152675; PMID:3303254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M26247; NID:g204145; PIDN:AAA41162.1; PID:g204146
C;Keperfamly: cosquitation factor X; RGF homology; Gla domain homology; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;56-282/Domâin: trypsin homology (fragment) <TRY>
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C;Keyberfanly, cosquistion factor X; EGR homology; Gla domain homology; trypsin homology
C;Keywords, hydrolase; serine proteinse
P;59-285/Domain: trypsin homology (fragment) <TRY>
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C.Species: Cavia porcellus (guinea pig)
C.Dere: Q2-Ud.-1996 #segmence_revision 02-Uul-1996 #text_change 22-Jun-1999
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Best Local Similarity 100.0%; Score 46; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 0.11,
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.1;
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A.Stacus: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-282 <RES>
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A). Status: preliminary; translated from GB/EWBL/DDBJ A). Redictive: preliminary; translated from GB/EWBL/DDBJ A). Residues: 1-265 < RES>
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Matches 9; Conservative
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Cibetes: 11-Dec-1992 Heequence revision 30-Jun-1987 Htext change 15-Sep-2000
Cibete: 11-Dec-1992 Heequence revision 30-Jun-1987 Htext change 15-Sep-2000
Cibete: 11-Dec-1992 Heequence revision 30-Jun-1987 Htext change 15-Sep-2000
R.Yoshitake: 8: Schach, B.G. Footer, D.C.; Davie, E.W.; Kurachi, K.
R.Yoshitake: 8: Schach, B.G. Footer, D.C.; Davie, E.W.; Kurachi, K.
A.Title Nocleotide sequence of the gene for human factor IX (antihemophilic factor B).
A.Reference number: A00922; MUID:86000558; PMID:2994716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule Type: DNA
A; Molecule Type: DNA
A; Molecule Type: DNA
A; Ctross-references: GB; KO2402; NID: G182612; PIDN: AABS9620.1; PID: G182613
B; A; Ctross-references: GB; KO2402; NID: G182612; PIDN: AABS9620.1; PID: G182613
B; Asson, D. S; Cthoo, KH; Rees, D. J. G.; Glannelli, F.; Gould, K.; Huddleston, J.A.; Brc.
B; MED 01. 3; 1053-1060, 1984
G192612 G192612 G192709; MUD: 84356100; PMID: G329734
A; Reference number: A37709; MUD: 84356100; PMID: G329734
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Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat ;Reference number: A22673; MUID:85190593; PMID:3857619
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More: the authors translated the codon ACA for residue 29 as Tyr Poletos?

Jave, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstos?

March Categories Res. 11, 2324-2355, 1937-1980; Palland, A.; Kohli, V.; Findeli, A.; Tolstos?

Title: Isolation of a human anti-hemophilic factor IX cDNA clone using a unique S2-ba-

Accession: A21337; WUID:83220788; PMID:6687940
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Alcoss-references: GB-000137, NID-19182610, PIDN: AAA52763.1, PID-19182611
Ridagadesewaram, P., Lawellb, V. NID-19182610, Ridagadesewaram, P., Lawellb, V. NID-19182610, Ridagadesewaram, P., Lawellb, V. NID-19182610, Ridagadesewaram, P., Lawellb, V. NID-1918261, Robert Callandesewaram, P., Reference mand Characterization of human factor IX cDNA: identification of Taq.I Alfatelernce mumber: AA7546; MUID:84300526; PMID:6089357
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Residues: 1-12, '8', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356,'A'
A;Crose-references: 08:J00136; NID:9185608; PIDN:AAA30726.1; PID:9182609
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SRetnem, P.H.; Berlin, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, 100d 72, 1074.1076; 1388
Title: The putative factor IX gene promoter in hemophilia B Leyden. **Reference number: AJ0511; MUID:88327116; PMID:3416069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rroc. Nati. Acad. Sci. U.S.A. 79, 6461-6464, 1982
Vittlei Isolation and characterization of a CDNA coding for human factor
*\Reference number: A30623; MUTD:81065193; PMID:8959130
                                                                                                      coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human N/Alternate names: antihemophilic factor B; Christmas factor
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A,Cross-references: GB:M35672
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Residues: 1-193,'T',195-461 <MCG>
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Residues: 1-461 <ANS>
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Residues: 8-24 <REI>
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                                    Molecule (1909 - MRM)

A; Mesidens 1-422 - AME.

A; Cross-references: GB:M33826; NID:g163949; PIDN:AA30844.1; PID:g163950

A; Cross-references: GB:M33826; NID:g163949; PIDN:AA30844.1; PID:g163950

A; Cross-references: GB:M33826; NID:g163949; PIDN:AA30844.1; PID:g163950

C; Seperfemily; coaguiation factor X; EGF honology; Ga domain homology; crypsin homology
C; Seywords: beta-hydroxyaspartic serid; blood coaguiation binding; carboxyglutan
F; 22-40/Domain: Gardence #status predicted <RGO
F; 22-40/Domain: Gardence #status predicted <RGO
F; 42-44/Domain: Gardence #status predicted <RGO
F; 90-121/Domain: Gardence #status predicted <RGO
F; 90-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127-163/Pomain: ERF Nonoiday -EED.
F-128-445/Domain: ERF Nonoiday -EED.
F-46-47,54,50-90-105-56,66,69/72,75,79/Modified site: gamma-carboxyglutamic scid (Glu) #6
F-57-62,90-101,95-110,112-111,127-118,134-148,155-65,177-26,243-259,373-387,396-426/01
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.;Rosedues: 168-362, 0.364-387, 11,389-451 <RES>
.;Rosedues: 168-362, 0.364-387, 11,389-451 <RES>
.;Coment: This protein plays a critical role in bload coagulation.
.;Comment: This protein plays a critical role in bload coagulation.
.;Comment: This protein plays a critical role in bload coagulation.
.;Reywords: beca.hydroxyasparic. acid; bload coagulation; calcium binding; carboxygluran
.;Reywords: beca.hydroxyasparic. acid; bload coagulation; calcium binding; carboxygluran
.;1-16/Domain: signal sequence (fragment) #steutus predicted <SIG>
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52-5452/Domain: trypain homology <EG2>
61.42,42,45,14,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #8
65-57,85-95,90-105,107-116,122-133,129-143,145-159,166-333,250-266,380-394,405-433/Dig
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Reference number: 146580; MUID:90152675; PMID:2303254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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.Jabre: 07.56p-1990; Hequence_revision 07-Sep-1990 #text_change 16-Jul-1999
.Accession: J09019; 149667
.Mu. S.M.: Stafford, D.W.; Ware, J.
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A.Filte: Deduced amino acid sequence of mouse blood-coagulation factor A.Filte: Deduced amino acid sequence of mouse 1900189; MUID:90215309; PMID:2323576
A.Accession: JO0419
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    mouse (fragment)

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Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation factor IXa (EC 3.4.21.22) precursor
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Sarkar, G.; Koeberl, D.D.; Sommer, S.S.
momics 6, 133-143, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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Residues: 1-459 <WUS>
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Matches 9; Conserv
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A, Experimental source: liver

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Rivorita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
B. Biol. Chem. 259, 588-5704, 1384
A.Fitle: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bindin.
A.Reference number: A37543; MUID:84185715; PMID:6425296
A.Contents: annotation; calcium binding
Rivorites, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
                                                                                                                                                                                                                                                                                                                                   F;226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental
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C.Species: Oryctolague cuniculus (domestic rabbit)
C.Dates 14 Feb. 1977 #sequence_revision 14 Feb.1997 #text_change 22 Jun-1999
C.Accession: 146712
R.Satkar, G.; Kooberl, D.D.; Sommer, S.S.
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A;Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:119900; OMIM:306900
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A/AND.caule Type: DNA
A/AND
                                                                                                                                                                                                                                                          A:Wolecule type: protein

Headsdues 47-22, YX, 55-60, YX, 52, YXX, 55 <THA>

R:Wolvallen, B.A.; Fulfakwa, K.; Kisiel, W.

A:Title The occurrence of beat-hydroxyaspartic acid in the vitamin K-dependent blood companies. A20274, WUID:83309813; PWID:6888526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Molecule type: protein
Residues: 105.109, W. 1.11-115 «MCM»
Ryseidues: 105.109, W. 1.10-115 «MCM»
Ryseidues: 105.109, W. MUID: 88166735; PMID: 3280312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Chatacterization of recombinant human Factor IX expressed in transgenic mice an
Reference number: $12088; MUID:91006024; PMID:2209546
A;Accession: $12088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolceule type: proceen
A:Residues: 29-63 -GAL.
A:Note: processed forms expressed in recombinant system
A:Achlarc, 7: Perraud, F.; Delemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien,
EMBO U. 9, 2395-3301, 4990
R/Tharakan, J.; Strickland, D.; Burgess, M.; Drohan, W.N.; Clark, D.B.
Vox Sang, 58, 21-29, 1990.
Aritle: Development of an immunoaffinity process for factor IX purification.
A.Reference number: A60486; MUID:90194857; PMID:2316207
A.Accession: A60486
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A, Residues: 1-68 <JAL>
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A;Cross-references: GB:chr_I; PIDN:AAC64633.1; PID:g3319446; GSPDB:GN00019; CESP:Y23H5A

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Gaps

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trypsin-like proteinase 1 (BC 3.4.21.-) precursor - imperfect fungus (Metarhizium aniso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Metarhizium anisopilae
C.Species: Metarhizium anisopilae
C.Species: Metarhizium anisopilae
C.Species: Metarhizium anisopilae
C.Speciesion: JG4517; 549329
C.Shocession: JG4517; 549329
S.Smithkon, S.L.; Paterson, I.C.; Bailey, A.M.; Screen, S.E.; Hunt, B.A.; Cobb, B.D.; C.
Gene 166, 161-165 1986
A;Fitle: Cloning and characterisation of a gene encoding a cuticle-degrading protease f:
A;Reference number: JC4517; MUID:96105219; PMID:8529802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         citrate synthase [imported] - Agrobacterium tumefaciens (strain CS8, Dupont) plasmid AT Spacies, agrobacterium tumefaciens C;Date: 11-dan-2002 #sequence_revision 11-dan-2002 #text_change 11-Jan-2002 C;Accession: AB3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A;Fille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Acetence number: AB2577; PMID:11743193
A;Accession: AB3197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1.434 «KUR»
Kross-references: GB:ARD008687; PIDN:AAL45995.1; PID:g17743749; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-254 <SM2>
A;Cross-references: EMBL:X78875; NID:g556656; PIDN:CAA55477.1; PID:g556657
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CKEWPACG: endolamni reticulum; bydzolame; serine proteinase
F1-12-17.Domain: signal sequence #status predicted <RIG-
F13-23/Domain: propeptide #status predicted <RBC-
F13-23/Product: trypsin-like proteinase #status predicted <MAT>
F102-25/Product: trypsin-like proteinase #status predicted <MAT>
F102-2209/Active site: H18, App, Ser #status predicted
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A:Note: submitted to the EMBL Data Library, April 1994
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 73.9%; Score 34; DB 2; Similarity 85.7%; Pred. No. 25; 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                        ..
7
                                                                                                                                                                                                                                                 Score 36; DB 2
Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                        78.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Introns: 86/3; 149/2
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                                                            C,Genetics:
A,Gene: Y23H5A.7
A,Map position: 1
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CiSpeciaes; infectious laryngotracheitis virus
CiSpeciaes; infectious laryngotracheitis virus
CiSpeciaes; infectious laryngotracheitis virus
CiSpeciaesion: S13444; A43675
CiAccession: S13444; A43675
Richtiffin, A.M.
Richti
Genomics 6, 133-143, 1990
A;Title: Direct sequencing of the activation peptide and the catalytic domain of the fact A;Title: Direct sequencing of the activation peptide and the catalytic domain of the fact A;Reference number: 146580, MUID:90152675; PMID:2303254
A;Recession: 146712
A;Recession: 146712
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                            A;Residues; 1275 <53K.

A;Residues; 1275 <53K.

C;Guperferences: Galiv2234; NID:g165020; PIDN:AAA31251.1; PID:g165021

C;Guperfamily; coegulation factor X; EGF homology; Gla domain homology; trypsin homology

F;49-275/Domain; trypsin homology (fragment) <1RV>
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**Tritle: Geneme sequence of the nematode C. elegans: a platform for investigating biolog A. Materence number: A75000, MID:99069613, PMID:981916
**A. Note: see websites genome. Mustl. edu/gsc/C. elegans/ and www. sanger.ac.uk/Projects/C.ele A. Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A. Mccession: H87720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Spæcies: Cenorhabditis elegane:
Pates: 10-May-2001 #Sequence_revision 10-May-2001 #text_change 10-May-2001
Accesson: M87729 | April 10-May-2001 #text_change 10-May-2001 
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21;
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A.Epperlmental source: etrain Thorne
C.Superfamily: varicells-zoster virus gene 33 protein
C.Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
0.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 42; DB
100.0%; Pred. No. 0.6
ive 0; Mismatches
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66.7%; Pred. No.
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Matches 6; Conservative
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Best Local Similarity
Matches 8, Conserv
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A;Molecule type: DNA
A;Residues: 1-909 <STO>
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Gaps

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us-09-851-422b-1.rpr

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C;Accession: I40186; 841295
Trinh, S.; Haggoud, A.; Reyset, G.; Sebald, M.
Microbiology 141, 927-935, 1995
A;Trille: Plannids pIP419 and pIP421 from Bacteroides: 5-nitroimidazole resistance genes
A;Frille: Plannids pIP419 and pIP421 from Bacteroides: 5-nitroimidazole resistance genes
A;Freeselon: I40184; MUID:95291442; PMID:7773395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X76949; NID: 9440383; PIDN: CAA54271.1; PID: 9440385
Score 34; DB 1; Length 2347;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2; Length 70;
Pred. No. 12;
3; Mismatches 0; Indels
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A;Wolecule type: DNA
A;Residues: 1-70 cRES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 1169b - Bacteroides fragilis
                                                                                                                          0; Mismatches
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       73.9%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
       Query Match 73.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                              309 LVDEAHCLR 317
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Job time : 17.75 secs
                                                                                                                                                                                                                       1 LVDRATCLR 9
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A,Fibre: the difference after residue 2245 result from the authors' misinterpretation of
R,Birchmeiter, G.; Birnbaum, D.; Waitches, G.; Fasano, O.; Wigler, M.
Mol. Cell. Biol. 6, 3109-3116, 1986
A,Title: Characterization of an activated human ros gene.
A,Reference number: A2421, MUD10:97064625, PMID:378523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Human c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma virus encode
Thefetence number: A2522; MUID:87064611; PMID:3023956
A.Accession: A35223
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Map position: 642-642-642.
Introne: 1853/1, 1863/1; 1956/2; 1980/3; 2002/2; 2004/3; 2018/2; 2145/2; 2190/2
Introne: 1853/1, 1863/1; 1956/2; 1980/3; 2002/2; 2004/3; 2018/2; 2145/2; 2190/2
Supertennily: kinase-related procedin rosi LDL receptor YWTD-containing repeat homology;
Keywords: ATP, ansae-related procedin rosi LDL receptor YWTD-containing protein
15 - 54/Nomin: signal sequence #status predicted 4430.
37 - 231/Recoduct: Kinase-related procedin Rosi Histatus predicted <a href="https://doi.org/10.1007/pic.2007-10.1007/">https://doi.org/10.1007/pic.2007-10.1007/</a>
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1951-1958/Region: procein kinase Arb-bindig motif
52,114,123,324,352,471,607,628,706,714,732,939,581,1015,1087,1090,1211,1272,1330,1458,
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F;2110,2114,2115/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat
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|Residues: 1854-2261, A., 226-2147 cBL2.
|Cross-references: GB:M13880, NID:G337482, PIDN:AAA36580.1; PID:G337483
|Experimental source: tumor cells | Experiment source; tumor cells | Experiment source; source; concegene was formed by DNA rearrangement involving fusion of at least stored.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wh.Alternate names: procein-tyrosine kinase mcf3 (activated ros-1)
W.Contains: procein-tyrosine kinase (EC 27.1.112) ros-1
C.Specias: Homo sapiese (man)
C.Specias: Homo sapiese (man)
C.Date: 31-Dec-1998 Heaquence revision 07.0ct-1994 #text_change 11-Jun-1999
C.Date: 31-Dec-1998 Heaquence revision 07.0ct-1994 #text_change 11-Jun-1999
C.Accession: ASS12, ASS12, ASS12, Margler, W.
FRIETCHENEER, C., O. Wall, K., R., M., Margler, W.
FRIETCHENEER, C., C., C., M., R., M., Margler, M.
Froc. Next. Acad. cct. U.S.A., 87, 479-400, 1990
A.FILLER Characterisation of Ros. Cons. Econ. a human glioblasroma cell line.
A.Reference number: ASS12, MUDD: 90280463; PMID:332399
                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37-1859/mcduct. Attacel latarcut products of status pressured von 37-1859/mcduct. Attacel latarcut producted carry as 27-1869/momain: LDL receptor WWTD-containing repeat homology vWN-35-187-57/homain: LDL receptor WWTD-containing repeat homology vWN-37-187-79/homain: LDL receptor WWTD-containing repeat homology vWN-37-188-798/homain: LDL receptor WWTD-containing repeat homology vWN-38-1888/homain: LDL receptor WWTD-containing repeat homology vWN-891-888/homain: LDL receptor WWTD-containing repeat homology vWN-891-898/homain: LDL receptor WWTD-containing repeat homology vWN-898/homain: LDL receptor WWTD-containing repeat homology vWN-898/homain: LDL receptor WWTD-containing
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                                                                DB 2; Length 434;
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1884-2347/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Wolecule type: mRNA
Kresidues 1-2212, Nr.,2214-2227, OCr.,2229-2347 <BIR>A.Gross-refetences: GB:WA453
A.Gross-refetences: GB:WA453
A.Grossimental source glicoblastoma call line SW-1088
R.Watsushiment H.; Wang, L. H.; Shibuya, M.
MATSUSHIMENT H.; Shibuya, M.
                                                                                                                                                                            1; Mismatches
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A,Residues: 1790-2245,'KFDSSEFSSFRCTVN' <MA2>
A,Crose-references: GB:M13368
                                                                Score 34;
Pred. No.
                                                                73.9%;
                                                                                                                   Best Local Similarity 66.7
Matches 6; Conservative
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                                                                Query Match
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Gape

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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

May 6, 2003, 15:01:10 ; Search time 18 Seconds (without alignments 43.143 Million cell updates/sec Run on:

US-09-851-422B-1 Title: Perfect score:

1 LVDRATCLR 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328255 Total number of hits satisfying chosen parameters:

328255 seqs, 86286685 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PUBCOMB. pep . . Central (products) (pubpss/1808 PRECOME, pep (cgn2 6 products) (pubpss/1808 PRECOME, pep (cgn2 6 products) (pubpss/1808 PRECOME, pep (cgn2 6 products) (pubpss/1801 PRECOME, pep /cgn2_6/picdestal/lpinpas/PCTN New PUB. /cgn2_6/picdestal/lpinpas/PCTN New FUB. /cgn2_6/picdestal/lpinpas/New FUB. /cgn2_6/picdestal/lpinpas/New FUB. /cgn2_6/picdestal/lpinpas/New FUB. /cgn2_6/picdestal/lpinpas/New FUB. Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 46600, A	Sequence 5, Appli	Sequence 3, Appli	Secuence 2, Appli	Sequence 351, App	Seguence 2, Appli	Secuence 188, App	Sequence 35244, A	Sequence 38, Appl	Sequence 120, App	Sequence 65, Appl	Sequence 1, Appli	Sequence 29, Appl	Sequence 362, App	Sequence 13, Appl		Sequence 312, App	Sequence 366, App	Semience 311. Ann
	ID	US-09-864-761-46600	US-10-132-829-5	US-09-884-901-3	US-09-118-748-2	US-10-012-542-351	US-09-821-255-2	US-10-001-843-188	US-09-864-761-35244	US-10-117-323-38	US-09-753-436-120	US-10-047-542-65	US-09-753-436-1	US-09-919-172-29	US-10-012-542-362	US-09-870-162A-13	US-09-886-055-205	US-09-731-872-312	US-10-012-542-366	US-09-731-872-311
		្ន	6	9	10	6	9	12	10	6	10	6	10	10	6	10	10	10	6	10
	Query Match Length DB	181	461	461	415	101	228	44	83	252	434	547	547	2125	24	223	338	382	429	466
*	Query Match	100.0	100.0	100.0	89.1	71.7	71.7	69.6	9.69	9.69	9.69	9.69	9.69	9.69	67.4	67.4	67.4	67.4	67.4	67.4
	Score	46	46	46	41	33	33	32	32	32	32	32	32	32	31	31	31	31	31	31
	Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

00 9 10 0 10 0 10 0 10 0 10 0 10 0 10 0	US-100-12-542-36 US-09-572-404B-11 US-09-572-404B-11 US-09-57-404B-11 US-100-55-817-6 US-100-645-815-4 US-100-645-815-4 US-100-645-815-4 US-100-645-815-4 US-100-1045-815-815-4 US-100-1045-815-815-4 US-100-1045-815-815-815-815-815-815-815-815-815-81	Sequence 365, App Sequence 2, Appli		Sequence 660, App	Sequence 2, Appli	Seguence 10, Appl	4	626, 7	Seguence 626, App	Sequence 34304, A	Sequence 2, Appli	Sequence 46, Appl	Sequence 3, Appli	Sequence 16, Appl	Sequence 28, Appl	Sequence 1, Appli	4	-	Seguence 1749, Ap	Seguence 1143, Ap	Sequence 36792, A	Sequence 1, Appli	Sequence 12, Appl		Sequence 2, Appli
	4.7.7.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	US-10-012-542-365 US-10-167-264-2	US-09-572-404B-1740	S				US-10-092-154-626		US-09-864-761	US-10-224-414-2	US-10-108-915-46		_	_	_	ם	2 US-10-078-929-168	US-09-572-404B-1749	US-10-083-357-1143	US-09-864-761-3			US-09-792-793A-14	US-10-141-965-2
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ALIGNMENTS

Sequence 46600, Application US/09864761
Parent No. USZODOŽOGATGAAA
GENERAL INPORMATION: Natron G.
APPLICANT: Penn, Natron G.
APPLICANT: Mank, David R.
APPLICANT: Hanes, Pavid R.
APPLICANT: Hanes, Pavid R.
APPLICANT: Onen, Wensheng JS-09-864-761-46600

TITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INTERPRESENCE: Acenida-X-1.

TITLE OF INVERTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acenida-X-1.

CURRENT PALLOATON WUMBE: US (9/864,761

CURRENT FILING DATE: 2000-105-23

PRIOR PILING DATE: 2000-105-23

PRIOR PILING DATE: 2000-106-23

PRIOR PILING DATE: 2000-106-30

PRIOR PILING DATE: 2000-106-32

PRIOR PILING DATE: 2000-106-32

PRIOR PILING DATE: 2000-106-32

PRIOR PILING DATE: 2001-106-32

PRIOR PILING DATE: 2001-106-33

PRIOR PILING DATE: 2001-106-33

PRIOR PILING DATE: 2001-106-33

PRIOR PILING DATE: 2001-106-33

PRIOR PILING DATE: 2001-10-30

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APPLICATION NUMBER: 60/090,112
DATE: 1998-06-22
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FILING DATE: EARLIER FILING DATE: 1999-06-22
APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 46; DB 10; Length 461; 100.0%; Pred. No. 0.46;
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TITLE OF INERTION: 94 Human Secreted Proteins
TITLE OF INERTION: 94 Human Secreted Proteins
TITLE OF INERTION: 94 Human Secreted Proteins
CURRENT FILINO DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US/10/12,542
PRIOR APPLICATION NUMBER: BALIER APPLICATION NUMBER: 09/
PRIOR FILINO DATE: BARLIER PEPLICATION NUMBER: 60/
PRIOR PRIOR PAPLICATION NUMBER: EALIER PEPLICATION NUMBER: 60/
PRIOR PRIOR PELINO DATE: 1998-06-16
PRIOR PELINO DATE: BARLIER PEPLICATION NUMBER: 60/
PRIOR PELINO NUMBER: BARLIER PEPLICATION NUMBER: 60/
PRIOR PELINO NUMBER: BARLIER PEPLICATION NUMBER: 60/
PRIOR PELINO NUMBER: BARLIER PERIOR DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: US 60/212,902 PRIOR FILING DATE: 2000-06-20 NUMBER OF SEQ 1D NOS: 18 SOFTWARE: Patentin version 3.0 SEQ 1D NO 3 LENGTH: 461
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Publication No. US20030044851A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                       ORGANISM: HomoSapien
US-09-884-901-3
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GENERAL INFORMATION:

APPLICANT: Chien, Kenneth R.

APPLICANT: Chien, Kenneth R.

APPLICANT: Hobilisma, Mashiko

TITLE OF INVENTION: Welch of treat hemophilia by hepatic gene transfer of Factor VII

TITLE OF INVENTION: Welch of treat hemophilia by hepatic gene transfer of Factor VIII

TITLE OF INVENTION: Welch of treat hemophilia by hepatic gene transfer of Factor VIII

TITLE OF INVENTION: With versic vector

CURRANT APPLICATION WUMBER: 1001-04-25

PRIOR FLITLE DATE:

NUMBER: OF SEC ID NOS: 5

SOFTHARE: PRICHILIN OFFICE OF SEC ID NOS: 5

LINGTHARE: ASIGNATION OFFICE OF
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Patent No. US2000076798A1
RESERVATION: MAP. Carol
APPLICANT: NAV. MARK
TITLE OF INVESTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
FILE REPRESENCE: US/09/884,901
CURRENT APPLICATION NUMBER: US/09/884,901
CURRENT APPLIATION DATE: 2010-06-18
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FEATURES, SIGNAL = 2.5
OTHER INFORMATION: SST HUMAN HIT: T28608.1, EVALUE 3.000-36
OTHER INFORMATION: SWISSPROT HIT: P00740, EVALUE 1.000-107
US-05-64-761-46600
                               PRIOR FILMO DARE: 2001-01-30
PRIOR PLING DARE: 2001-01-30
PRIOR PLING DARE: 2001-01-30
PRIOR PLING DARE: 2000-09-31
PRIOR PLING DARE: 2000-06-30
PRIOR PLING DARE: 2000-06-30
PRIOR PLING DARE: 2001-01-29
PRIOR PLING DARE: 2001-01-29
NUMBER OFFSER ADDITIONOS: 49117
SOFFWARE: Annomex Sequence Listing Engine vers: 1.1
SOFFWARE: Annomex Sequence Listing Engine vers: 1.1
     APPLICATION NUMBER: PCT/US01/00670
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Publication No. US20030044982A1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                 DB 12; Length 44;
20;
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OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
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                                                                                                                                                                                                                                                    Mismatches
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Patent No. US20020048763A1
                                                                                                                                                                 69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 6; Conservative
           ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-843-188
                                                                                                                                                                                                                                                                                                                                                                               7 LVERAVCL 14
                                                                                                                                                                                                                                                                                                                                  1 LVDRATCL 8
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APPLICANT: Acidestey, Robert
APPLICANT: Sun, Vongwing
APPLICANT: Sun, Vongwing
APPLICANT: Sun, Vongwing
APPLICANT: Tolur Chenghua
APPLICANT: Tolur Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and 10 TRENE PRETANTE: DES. 2016 71.12.20
CURRENT FILING DATE: 2010-11.20
PRICER PRELICATION WOMER: 607-249, 992
PRICER PLILING DATE: 2000-11.20
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                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 101;
30;
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GREEAL INFORMATION
APPLICANT: McC.16 Bun
APPLICANT: Cecl.18 R.Y. Sun
APPLICANT: Cecl.10 R.Y. Sun
APPLICANT: Cecl.10 R.Y. Sun
APPLICANTION WHERE: US/09/81,255
CURRENT APPLICATION WHERE: 05/075,328
REIOR APPLICATION WHERE: 199-02-20
REIOR APPLICANTON WHERE: 199-02-20
REIOR APPLICATION WHERE: 199-02-20
REIOR APPLICANTON WHERE: 199-02-20
REIOR APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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PRIOR FILIMG DATE: EARLIER FILING DATE: 1998-06-22 UNMER OF SEQ 1D NOS: 532 SOFFWARE! Patentin Ver. 2.0 SEQ 1D NO 351 LEWSTH: 101
                                                                                                                                                                                                                                                                                                                                                              Query Match 71.7%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 30; Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 188, Application US/10001843
Patent No. US20020132255A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09821255
Patent No. US20020081293A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 188
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macina, Roberto
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APPLICANT: Salceda, Susana
                                                                                                                                                                                                        rype: PRT
CORGANISM: Homo sapiens
US-10-012-542-351
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Matches 6; Conserv
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 DRATCL 8
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US-09-821-255-2
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GERBEAL INFORMATION

APPLICANT: LARGECK, AMES W.
APPLICANT: WROOPF, KEITH L.
TITLE OF INVENTION: VOUE IMPUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISBASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
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Pred. No. 2.1e+02;
1, Migmatches 0; Indels
                  COMPUTER: IBM PC compartible
ODERATING SISTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/09/753,436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILLE CONTRIBUTION AND WASTERLAND VISSANDE CURRENT PREJECTION WOMBER: US/10/04/542 CURRENT FILING DATE: 2001-10-26 PRIOR PELCATION WOMBER: PCT/US01/13932 PRIOR FILING DATE: 2001-04-38 PRIOR PALICATION WOMBER: 60/200,298 PRIOR APPLICATION WOMBER: 60/200,298 WASTERLING DATE: 2000-04-28 WOMBER OF SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
FILIN
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FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 65, Application US/10047542
Patent No. US20020168367A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION
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TELEFAX: (312) 474-0448
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acida
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
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292 IDRATC 297
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EST_HUMAN HIT: AU141284.1, EVALUE 5.00e-31
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Pred. No. 38;
1; Mismatches 1; Indels
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Pred. No. 1.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
N: EXPRESSED IN PETAL LIVER, SIGNAL = 1.
N: EXPRESSED IN PLACENT, SIGNAL = 2.1
N: EXPRESSED IN PLACENT, SIGNAL = 1.2
N: EXPRESSED IN HEART, SIGNAL = 1.2
N: EXPRESSED IN HEART, SIGNAL = 1.4
N: EXPRESSED IN HEART, SIGNAL = 1.4
N: EXPRESSED IN BRAIN, SIGNAL = 1.4
N: EXPRESSED IN BRAIN, SIGNAL = 1.5
THE SIGNAL = 1.5
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APPLICANT: Gallatin, M. Michael
APPLICANT: Gallatin, Rosemay
ITILE OF INVESTION: ICAM-Related Materials and Methods
WOMER OF SEQUENCES: 120
CORRESPONDERE ADDRESS: 120
ADDRESSES: MATERIALL, O'TOOLE, Gerstein, Murray & Borr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
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CODWIN: United States of America
ZIP: B6606-6402 SATE:
COMPURE READABLE FORM:
MEDIUM TYPE: Ploppy disk
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209-733-436-120

; Sequence 120, Application US/09753436

; Patent No. USZODIOZ22293A1
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Publication No. US20030054993A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.6%;
Best Local Similarity 75.0%;
Matches '*6; Conservative
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Best Local Similarity 66.77
6; Conservative
                                                 OTHER INFORMATION: ED OTHER INFORMATION: ED
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CITY: Chicago
STATE: Illinois
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US-10-117-323-38
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LENGTH: 252
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Gaps
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Substantian No. USCO03044455A1

Substantian No. USCO030044455A1

Substantian No. USCO030044455A1

Substantian No. USCO030044455A1

ATTLE OF INTERNATION OF A Human Secreted Proteins
FILING DATE: OF ADDRESS. US/10/012,542

CURRENT FILING DATE: SANLIER PRESIDENTIAN OF ADDRESS. GO/089,507

PRIOR FILING DATE: SANLIER PRESIDENTIAN OF ADDRESS. GO/089,507

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,509

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,509

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,509

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,510

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,510

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,510

FRIOR FILING DATE: SANLIER PAPILCATTON NOMER: GO/089,510
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Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 69.6%; Score 32; DB 10; Length 547; Best Local Similarity 83.3%; Pred. No. 2.6e-06. Matches 5; Conservative 1; Mismatches 0; Indels Matches 5; Conservative 1; Mismatches 0; Indels
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OTHER INFORMATION: Incyte ID No. US20020119463A1 3774181CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09919172
| Retent No. US/02020119463A1
| GENERAL INFORMATION:
| APPLICANT: Frais, Mary
| APPLICANT: Thirds, Mary
| TITLE OF INVENTION: PROSTATE CANCER MARKERS
| TITLE OF INVENTION: PROSTATE CANCER MARKERS
| CURRENT FILLING DART: 2001-07-30
| RIOR APPLICATION NUMBER: 60/221469
| 
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                                                         : 547 amino acids
amino acid
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Matches 7, Conservative
SECUENCE CHARACTERISTICS
                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 1946 LVDRITALR 1954
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402 IDRATC 407
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US-10-012-542-362
                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-09-753-436-1
                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-919-172-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Warnhall O'Toole, Gerstein, Murray & Borun STREET: G100 Sears Tower, 233 South Wacker Drive CTFY. C1016 Sears Tower, 233 South Wacker Drive CTFY. 1111nois SCHWITZ: 1111nois CONFRY. 1111nois Schoeled of America COMPUTER RRADALS FORM: COMPUTER RRADALS FORM: COMPUTER TEACH STREAM 
                                                                                                                                                                                                                                                                                                                                                                                                          Omery Match 69.6%; Score 32; DB 9; Length 547; Beet Local Similarity 83.3%; Pred. No. 2.6e-60; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APLICANT: Gallatin, W. Michael
APLICANT: Gallatin, N. Michael
APLICANT: Vazeux, Nosemay
TITLE OF INVENTION: TCAM-Related Materials and Methods
WIMMER OF SEQUENCES: 120
CORRESPONDENCES: 120
CORRESPONDENCES: 120
AUDRESSEE: Marshall, O'Toole, Gerstein, Murray & Boru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE.

PELLING DATE.

PELLING DATE.

ROUGH 1995

RIGHT OF JUN 1995

RIGHT OF JUN 1995

RIGHT OF JUN 1995

RIGHT OF JUN 1994

RILING DATE.

RELLING DA
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FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09753436 Patent No. US20010029293A1
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 IDRATC 407
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                                                                                                                                                                                                                                                                                       US-10-047-542-65
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US-09-753-436-1
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
PRIOR APPLICATION VNBER: EARLIER APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: EARLIER PILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PARTIENT PART: 2.0
SEQ ID NOS: 2.0
INDER: PART: 24
TYPE: PRT
ORGANISM: Amon sapiens
                                                                                                                                                                                                                                                                            Query Match 67.4%; Score 31; DB 9; Length 24; Beet Local Similarity 75.6%; Pred. No. 17; Metches 6; Conservative 1; Mismatches 1; Indels Matches 6; Conservative 1.
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12 LQDRASCL 19
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RESULT 15 US-09-870-162A-13

Sequence 13, Application US/09870162A

PREGRAM NO. US200042118A1

GENERAL INFORMATION: Bacining, Sabine
APPLICANT: Breining, Sabine
APPLICANT: Breining, Sabine
TITLE OF INVENTION: Phenol Induced Proteins of Thauera aromatica
TITLE OF INVENTION: Phenol INVENTION: Phenol INVENTION: Phenol INVENTION: Phenol INVENTION: DOING INVENTION: Phenol INVENTION: 2000-05-30

PRIOR APPLICATION NUMBER: 09516914

PRIOR PRIOR PRIOR PROS: 44

SOFTHAME: Microsoft Office 97

LENGTH: 201

LENGTH: 20 Query Match 67.4%; Score 31; DB 10; Length 223; Best Local Similarity 66.7%; Pred. No. 1.6e-02. Matches 6; Conservative 1; Wismatches 2; Indels Matches 6; Conservative 1; Wismatches 2; Indels TYPE: PRT ORGANISM: Thauera aromatica US-09-870-162A-13

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46 LITRAGCLR 54

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Search completed: May 6, 2003, 15:04:52 Job time : 19.3333 Becs

us-09-851-422b-1.rai

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7 14:15:01 2003
Wed May
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

May 6, 2003, 14:59:30 ; Search time 14.4 Seconds (Without alignments | 18.389 Million cell updates/sec Run on:

US-09-851-422B-1

1 LVDRATCLR 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

262574 Total number of hits satisfying chosen parameters: 262574 seqs, 29422922 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/ogn2 6/ptodata/1/iaa/SA_COMB.pep:*
/ogn2 6/ptodata/1/iaa/SCOMB.pep:*
/ogn2 6/ptodata/1/iaa/GA_COMB.pep:*
/ogn2 6/ptodata/1/iaa/GB_COMB.pep:*
/ogn2 6/ptodata/1/iaa/GB_COMB.pep:*
/ogn2 6/ptodata/1/iaa/GB_COMB.pep:* Issued Patents AA Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 11, Appl	Sequence 12, Appl	Sequence 48, Appl	1,	~	Sequence 2, Appli	H			Sequence 21, Appl	Patent No. 5521070	Sequence 44, Appl		Patent No. 5223425	No.	9	2,	7	~	~	Sequence 2, Appli	7	Sequence 120, App		8	Sequence 8, Appli	Sequence 1, Appli
;	ID	US-08-797-842-11	US-08-797-842-12	US-08-944-483-48	US-08-073-531B-1	US-08-295-411-2	US-08-955-471-2	US-08-766-288-1	PCT-US92-10242-2	US-08-742-877-2	US-09-053-871A-21	5521070-2	US-08-944-483-44	5223425-5	5223425-4	5223425-8	US-08-944-483-61	US-08-270-584A-2	US-08-568-031-2	US-08-765-192-2	US-08-966-319-2	US-09-153-304-2	US-09-199-793-2	US-08-487-113D-120	US-08-720-420A-120	US-09-240-915-8	US-09-591-435-8	US-08-314-615-1
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	Match Length DB	40	40	235	415	415	415	415	415	461	461	461	228	238	250	253	239	268	268	268	268	268	268	434	434	518	518	547
Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	71.7	71.7	71.7	71.7	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69	9.69
	Score	46	46	46	46	46	46	46	46	46	46	46	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32
Result	NO.	1	7	m	4	S	ø	7	æ	6	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27

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Gaps ;

Query Match 100.0%; Score 46; DB 2; Length 40; Best Local Similarity 100.0%; Pred. No. 0.019; Matches 9; Conservative 0; Mismatches 0; Indels

Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	3500, Ap	5223425	, Appl	Appli	
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	
US-08-314-362-1	US-08-473-981A-6	US-08-433-010-1	US-08-482-882-1	US-08-483-389-1	US-08-487-113D-1	US-08-473-503-1	US-08-483-932-1	US-08-474-087-6	US-08-720-420A-1	US-08-714-017-1	US-08-863-790-1	US-08-475-680-1	US-08-296-749-1	US-09-134-001C-3500	5223425-6	US-09-516-914-13	US-08-149-103-3	
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69	69	69	69	69	69	69	69	69	69	69	69	69	69	67.4	67.4	67.4	67.	
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ALIGNMENTS

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Sequence 11, Application US/08797842
Patent No. 292706
GENERAL INFORMATION:
APPLICANTY: Mertens, Koenrad et al.
TITLE OF INVENTION: Antibodies specific for a haemostatic protein,
TITLE OF INVENTION: their use for isolating intact protein, haemostatic compositi
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLIW TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
SOFTWARE: Microsoft Word for Windows 6
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/797,842
FILING DATE: 10-Feb-1997
CLASSIFICATION: 530
CLASSIFICATION 542
APPLICATION NUMBER: 06/781,691
FILING DATE: FEB-1997
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                           ADDRESSEE: Michaelson and Wallace
STREET: Parkway 109 Office Center, 328 Newman Springs
STREET: Road, P. O. Box 8489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Michaelson, Peter L.
REGISTRATON NUMBER: 30090
REPRENCE/DOCKET NUMBER: Stitching-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (908) 530-6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (908) 530-6584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 amino acids
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NO
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                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                      CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                         US-08-797-842-11
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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RESULT 1
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us-09-851-422b-1.rai

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NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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    Polymeric Conjugates

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ZIP: 11788

ZIP: 11788

WEDTUR TYPE: Diskette, 3.50 inch, 1.44 MD Storage COMPUTER: IBM Compatible OPERATING SYSTEM: DOS 6.0

SOFTWARE: MordPerfect 6.1

CARERAT PADICATION DATA:
CARRENT PADICATION DATA:
CARRENT PADICATION NOWERR: US/08/073,5318
                                                                                                                                                                                                                                                                                        COUNTRY: USA

COUNTRY INSA

IN SO 16064-3500

COMPUTER REAABLE FORM:

COMPUTER: IEEM Compatible

COMPATING STERM: OF WINDOWS Version 2.0

CORPRAGE FREESOR for Windows Version 2.0

COUNTRY APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 46;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6183.US.01
                                                                                                                                                                             ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08073531B Patent No. 5621039
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APPLICANT: HALlahan, et al.
TITLE OF INVENTION: Factor IX
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35,441
STEVEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 6:
TELECOMMUNISTROCKMATION
TELEPHONE: 847/935-1729
TELEPAX: 647/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: No. 6232456e
US-08-944-483-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: GALGANO & BU
STREET: 300 Rabro Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
3, Conservative
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APPLICANT: STROUPE, STEV
TITLE OF INVENTION: NOV
TITLE OF INVENTION: OF T
TITLE OF INVENTION: OF T
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GALGANO &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hauppauge
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||||
150 LVDRATCLR 158
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                                                                                                                                                                                                                                                           IL
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-073-531B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
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                                                                                                                                                                                                                                                                            Antibodies al Antibodies pecific for a haemostatic protein, their use for isolating intect protein, haemostatic compositic of proteolytic cleavage products of the protein 16
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CURRENT APPLICATION DAYs.
APPLICATION WUMBER: US/08/797,842
FILING ADSIFTANTON WINGER: US/08/797,842
CLASSIFTCHNS: 530
ADDITATION TOWN STATEMENT OF THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Michealeon and Wallace
STREET: Parkway 109 Office Conter, 328 Newman Springs
STREET: Road, P. O. Box 8489
STREET: New Jersey
STATE: New Jersey
ZTREE: 07701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA.

#PRICATION NUMBER: 00/381.891

#PRINKT AGRAT INFORMATION:
NAME: Wicheal Bon. Percer L.

REGISTRATION NUMBER: 30095

RESERRANCE DOCKET NUMBER: 5 ELICHING-5

TELECOMMUNICATION NUMBER: 8 ELICHING-5

TELECOMMUNICATION NUMBER: 8 ELICHING-5

TELECOMMUNICATION NUMBER: 9093390-6671
                                                                                                                                                                                                      Sequence 12, Application US/08797842
Patent No. 5932706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/08944483 Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COLPITTS, TRACEY L. FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (908)530-6584
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 amino acids
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MORTENS (CONTINE OF INVENTION: AntitITLE OF INVENTION: AntitITLE OF INVENTION: Of PUMBER OF SECURACES, 16
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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Best Local Similarity
Them 9; Conserve
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                                                         23 LVDRATCLR 31
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1 LVDRATCLR 9
                                                                                                                                            RESULT 2
US-08-797-842-12
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
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John H. Rolf Protease-Derived Polypeptides and Serine Protease-Derived Polypeptides and Anti-Peptide Antibodies, Systems and Therapeutic Methods for Inhibiting Coagulation
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ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
LOCATION: 1..15
LOCATION: 1..15 / note= "Factor IX Light Chain"
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Peptide"
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/955,471,
                                                                                                                                                                                                                                                                                                                                           TSRI263.0C1
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NOMBRE: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERRACE/ DOCKET NUMBER: TSRIZ63.0C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-06-95-471-2
Factors 2. Application US/08955471
Factors 2. Application US/089595471
Factors 2. Application US/08955471
Factors 2. Application US/0895471
Factors 2. Appl
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                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
                                22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 146..180
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 181..415
OTHER INFORMATION:
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                                     FILING DATE: 22
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-295-411-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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ADDRESSEE: Research Institute
'STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Johla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELEVANT RESIDUES IN SEQ ID NO: 1: FROM US-08-073-531B-1
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 415 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown to applicant
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08295411 Patent No. 5679639
                                                                                                                    TILING DATE:
ATTORNEY, AGRAT INFORMATION:
NAME: GALGARO & BURKE
REGISTATION WINDER: 30,735
REFERENCE, DOCKET NUMBER: 128-
TELECOMONICATION INFORMATION:
TELECOMONICATION SPE-610
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Orificin, John H.
APPLICANT: Mesters Rolf M.
APPLICANT: Mesters Rolf M.
TITLE OF INVENTION: Series
TITLE OF INVENTION: Anti-Pept
TITLE OF INVENTION: for Inhib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Cffice of Patent
ADDRESSER: Cffice of Patent
ADDRESSER: Research Institut
June 8, 1993
4: 525
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
PUBLICATION INFORMATION:
AUTHORS:
                           CLASSIFICATION: 525
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
CELL TYPE:
IMMEDIATE SOURCE:
LIBRARY:
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ORGANISM: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
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US-08-295-411-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hawpauge
STATE: New York
COUNTRY: USA
TOWNERS READABLE FORM:
COMPUTER: Diskette 3.50 inch, 1.44 Mb Storage
COMPUTER: HIM COMPACIBLE
COMPUTER: HIM COMPACIBLE
COMPUTER: HIM COMPACIBLE
COMPUTER: HIM COMPACIBLE
COMPUTER: Mortderfect 6.1
CURRENT APPLICATION DAYS
APPLICATION NUMBER: US/08/766,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1. Application US/08766288
Patent No. 5595040
GENERAL INFORMATION:
APPLICANT: HAllahan, et al.
TITLE OF INVENTION: Factor IX - Polymeric Conjugates
NUMBER OF SEQUENCES:
CORRESPONDING ADDRESS:
ADDRESSEE: GALGANO & BURKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LCCATION: 1..145 .
OTHER INFORMATION: /note= "Factor IX Light Chain"
PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 181..415
O'THER INFORMATION: /note= "Factor IX Heavy Chain"
US-08-955-471-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/ET: Region
LOCATION: 146..180
OTHER INFORMATION: /note= "Factor IX Activation
OTHER INFORMATION: Peptide"
                                                                                                                                  CLASSIPCATION:
ATTOWNEY/AGENT INFORMATION:
NAME:
NAME:
REGISTRATION THOMBER:
REGISTRATION THOMBER:
TELEPHONEY CATTOWNEY THOMBER:
TELEPHONEY CATTOWNEY THOMBER:
TELEPHONE:
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TELEPHONE:
TELEPHONE:
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FILING DATE:

CLASSIFICATION: 5.25

RAIGN APPLICATION DATA:

AFPLICATION NUMBER:

ATTOMETY AGANT INPORMATION:

NAME: GALGANO & BURKE
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GALGANO & BURKE
STREET: 300 Rabro Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
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Sequence 2, Application PC/TUS9210242
Sequence 2, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Official, John H.
APPLICANT: Mesters Roif Tring Protesse-Derived Polypeptides and TITLE OF INVENTION: Serial Fortesse-Derived Polypeptides and TITLE OF INVENTION: Anti-Peptide Anti-bodies, Systems and Therapeutic Methods TITLE OF INVENTION: Anti-Peptide Anti-bodies. Systems and Therapeutic MUMBER OF SEQUENCES. 10 CONTRIBUTION: Anti-Peptide Anti-bodies. Or Invention Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
STREET: A Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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APPLICATION NUMBER: PCT/US92/10242 FILING DATE: 19921118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 46; DB 2;
100.0%; Pred. No. 0.21;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM US-08-766-288-1
REGISTRATION WINBER: 30,735
RESPERBICE/COCKET NUMBER: 128-7 (DIV)
TELEBHONE (CATO, INFORMATION:
TELEBHONE: ($16) 562-6191
INPORMATION FOR SED TO NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION WHORER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAWE: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       TOPOLOGY: Unknown to applicant MOLECULE TYPE: -
                                                                                                                                                              LENGTH: 415 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
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Best Local Similarity 100.

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                       ANTI-SENSE: CORIGINAL SOURCE: ORGANISM: -
                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE: -
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VOLUME:
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Sequence 21. Application US/09053871A
Paperer No. 613595
GENERAL INCOMATION:
APPLICANT PINSKY, David J.
APLICANT Stem, David APLICANT Stem, David APLICANT Stem, David APLICANT Stem, Solumin, Robert A.
APLICANT SOLUMIN, Robert A.
APLICANT SOLUMIN, ROBERT A.
APLICANT SOLUMIN, ROBERT A.
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING TITLE OF INVENTION: STROKE OUTCOME.
FILE REPREDUCE: 5317-8
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PELLING DATE: 03-NOV-1982

APPLICATION NUMBER: 970,966

FILING DATE: 03-NOV-1982

RELING DATE: 03-NOV-1982
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                                                                                                                                 100.0%; Score 46; DB 3; Length 461; 100.0%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 46; DB 4; Length 461;
100.0%; Pred. No. 0.23;
iive 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1999-04-01
CURRENT FILING DATE: 1999-04-01
SOFTWARE: PatentIn Ver. 2.1
     LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity luv.v
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Matches 9; Conservative
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                                                                                                                                                                                                                                                   376 LVDRATCLR 384
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US-09-053-871A-21
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                                                                                        US-08-742-877-2
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                                                                                                                                    Query Match
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5521070-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALDABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PRESE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: TBM PC compatible
CLASSIFICATION NAMER: US/08/742,877
FILING DATE: 01-NOV-1996
FILING DATE: 03-NAY-1994
ATTOMEY/AGENT INPORMATION:
NAME: FLESHNER, RAZ E:
REGISTRATION NUMBER: 34,31
                                                                                                                                                                                                                                                                                               NAME/KEY: Region
LOCATION: 1..145
OTHER INFORMATION: /note= "Factor IX Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Region
| LOCATION: 181..415
| COTHER INFORMATION: /note= "Factor IX Heavy Chain"
PCT-US92-10244-2
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Factor IX Activation
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                          SCR0472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANY: CLARK, Anthony J.
TITLE OF INVENTION: DNA SEQUENCES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08742877
Patent No. 6046380
REGIEVATION WHERE: 34.153
REFERENCE/OCKET HIMBER: SCRC
TELECOMMUNICATION INVORMATION:
TELEPHONE: 6.19-554-6312
INPOMATION FOR SED ID NO: 2:
SEQUENCE GRAAACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2840
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  LENGTH: 415 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHERICAL: NO ANTI-SENSE: NO FRATURE:
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: Region
LOCATION: 146.180
OTHER INFORMATION: //
OTHER INFORMATION: PRATURE:
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ZIP: 20005-3934
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RESULT 14
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APPLICANT FULER, DEPREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
APPLICANT FULER R.
BARRY M. HHITE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 6; Length 238;
Pred. No. 38;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 6; Length 250;
Pred. No. 40;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 33; DB 6; Length 253; 66.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 00/277,963

FILMS DATE: 30-NOV-1986

PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
FILMS DATE: 30-NOV-1986

PRIOR APPLICATION NATA:
APPLICATION NA
                                              APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-WV-1988
PRIOR APPLICATION DATE: APPLICATION NUMBER: 43,203
FILING DATE: 02-APP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION WNBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION UNMER: 34,203
FILING DATE: 02-APF-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Matches 6; Conservative
CURRENT APPLICATION DATA
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Best Local Similarity 66.7
Matches 6; Conservative
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROGRAM
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FREGER NO. 5223425
FREGER NO. 5223425
FREY W. WHÎTE, TYLER R.
FRRY W. WHÎTE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
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DEBATING SYSTEM: DESTART OF SOFTWARE: FREEDS for Windows Version 2.0
CURRENT APPLICATION POWER: USA, 483
APPLICATION NUMBER: USA, 483
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APPLICANT: COUPTING: TRACEY L.
APPLICANT: COUPTING: TRACEY L.
APPLICANT: COUPTING: TRACEY L.
APPLICANT: RARANDON: BIONAD N.
APPLICANT: RARANDON: BIONAD N.
APPLICANT: STERNAR' REBY D.
APPLICANT: TILLE OF INVESTION: OF THE PROSTATION OF TH
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Patent No. 6232456
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ATTORNEY AGENT INFORMATION:
NAME: BECKET Cheryl I.
REDISTRATION NOMER: 35,441

REPERRINGE JOGGET NUMBER: 6183

TELECOMMUTCATION INPORMATION:
TELECOMMUTCATION INPORMATION:
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// MOLECULE TYPE: No. 6232456e

US-08-944-483-44
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SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acida
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 66.7
Matches 6, Conservative
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY: USA
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Search completed: May 6, 2003, 15:04:05 Job time : 16.4 secs

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Human 5' EST secre

Human Factor IX.

Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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Human Factor IX pr
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Human wild-type fa
Human factor IX (h
Protein of human f
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Amino acid sequenc
Propionibacterium
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ENV93/HTLV-1-IIIB'
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AAM41225
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AAM67720
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3-JUN-2000; 2000US-0690408.

21-SEP-2000; 2000US-023366.

21-SEP-2000; 2000US-033369.

04-OCT-2000; 2000US-033369.
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Human Factor-IX.
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                                                                                                              6, 2003, 14:57:44 ; Search time 40.95 Seconds (Without alignments) 20:266 Willion cell updates/sec
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1. (21102/goddata/geneseq/geneseqp-embl/AA1980.DAT: 1. (21102/goddata/geneseq/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseq/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseq/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseq/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqf/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqf/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqf/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqf/geneseqp-embl/AA1981.DAT: 1. (21102/goddata/geneseqf/geneseqp-embl/AA1991.DAT: 1. (21102/goddata/geneseqf
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              GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100*
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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AAB60289
AAR64266
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AAP40178
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Human brain expres Human bone marrow Peptide #1964 enco

Peptide #2014 enco Peptide #2043 enco Protein #1945 enco

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us-09-851-422b-1.rag

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Age-related gene regulation; liver-specific; gene expression; human factor IX; hBY; ABS', AB3', age-regulatable expression construct; antiesnee therapy, gene therapy; thrombosis; cardiovascular disease; diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in an age-related manner and/or in a layer-specific manner. The invention identifies regions of the human factor IX (NETX) gene, an a region of the human process (NPC) gene, which are age-related a regulatory sequences in the NETX age-related regulatory sequences are designated ABS (AAPS 6106) and ABS (AAPS 4019) and are found in the S' UTX (at position 2164-2165 of AAPS 4019) and are found in the S' 3485-3565 of AAPS 4018) respectively. These elements act synergistically
                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a smalle derived from human foetal laver. The single exon nucleic acid probes may be used for predicting measuring and displaying gene expression in samples derived from human feetal liver. The present sequence in a peptide encoded by a single exon nucleic-acid probe of the invention.

Mote: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic forme directly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New regulatory elements that control age-related gene expression, useful in gene therapy and for reducing Factor IX expression
                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                           Claim 27; SEQ ID NO 28643; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 46; DB 22; Length 181; Larity 100.0%; Pred, No. 0.43; Conservative 0; Mismatches 0: InAble '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human factor IX (hFIX) exon-encoded fragment, SEQ ID NO:12.
                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB60289 standard; Protein; 182 AA.
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 LVDRATČÍR 104
                                                                                                                                                                                                                                                                                                                    Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAFS4018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200075279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kurachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB60289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X44X8X00000000000X8
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The game ago related regulatory sequence is found in the 5'type and the state of th
to increase hFIX levels over the lifespan of an individual; however, they can independently exert effects on hFIX mRNA in an age-related manner, with ABS' acting to stabilise hFIX mRNA, and ABS' acting to increase hFIX mRNA levels, over time. ABS' also directs liver-specific expression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                age-related rise in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these diseases, in acreening for potential therapeutic agents and for studying normal processes such as ageing and gene expression. Fragments and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homologues of age-related regulatory sequences, are useful as probes to detect, isolate or identify other such sequences in samples. The present sequence represents a fragment of hFTX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
100.0%; Score 46; DB 22; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "gamma carboxy-glutamate-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor-IX; polymer conjugate; hemophilia-B; blood-clotting; coagulant; polyethylene glycol; PEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR64266 standard, protein, 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...46
'label= Gla_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 LVDRATCLR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Factor-IX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR64266;
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Modified-site

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Human Factor-IX is a single chain glycoprotein having the sequence given in AAR64266. Conjugates of Factor-IX with polymers such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Factor IX-non-antigenic polymer conjugates - useful for treatment of haemophilia B
                  note= "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "gamma-carboxyglutamic acid" 7..22
                                                                                                                           note= "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                       note= "gamma-carboxyglutamic acid"
                                                                                                                                                                                                                                                                                             note= "gamma-carboxyglutamic acid"
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                                                                     note= "gamma-carboxyglutamic acid"
                                                                                                                                                                                 note= "gamma-carboxyglutamic acid"
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note= "Pactor-XIa cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Factor XIa cleavage site"
196..412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "PEG attachment site"
[78..179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "PEG attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128..195
|label= Activation_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= EGF-like_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig. 1; 27pp; English.
                                                label= OTHER
                                                                                                                                                          abel= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilbert CW, Hallahan TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-036423/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ENZO-) ENZON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
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Gaps
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271..29
/note= "claim 6, page 137-138 describes an antibody
that reacts with Factor IX; fragments
316-330, 321-330, 395-409, 400-409 and
400-414 but not with fragment 271-222"
                                                                                                                                                                                                                                                                                                                                                                                                     PC; protein C; IX; Factor IX; X; Pactor X; PT; prothrombin; VII; Protor VII; CT; chymorrypsinogen; SP; serine processe; binding; exosite; catalytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "pref. PC polypeptide; claim 2, page 136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "pref. PC polypeptide; claim 2, page 136"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
                                                                    Length 412;
                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "pref. PC polypeptide; claim 2,
                                                                    16;
polyethylene glycol show reduced immunogenicity.
                                                               100.0%; Score 46; DB 16
100.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Factor IX light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Factor IX heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Factor IX activation"
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                              AAR35761 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "exosite 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "exosite 2"
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                                                                                                                                                                                                                                                                                                                                   24-SEP-1993 (first entry)
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                                                   Ouery Match
Best Local Similarity luv...
"has 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "p
321..330
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100..414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
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                                                                                                                                    1 LVDRATCLR 9
||||||||
327 LVDRATCLR 335
                                  412 AA;
                                                                                                                                                                                                                                                                                                                                                                     Factor IX (IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1993.
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                                                                                                                                                                                                                                                                                                   AAR35761;
                                  Sequence
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                                                                                                                                                                                                                              RESULT 4
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Christmas disease; therapy; haemophilia; factor IX; blood clotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by part of the sequence of human factor IX cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA cloning vehicles - useful in prodn. of factor IX polypeptide and of diagnostic probes for Christmas disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 46; DB 5; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
Matches 9; Conservative 0
                                                                                                                                                                                               Part of the sequence of human factor IX.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP40222 standard; Protein; 456 AA
                                                             AAP40178 standard; Protein; 456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NATR ) NATIONAL RES DEV CORP. (BROW/) BROWNLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83GB-0012491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82GB-0022485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83WO-GB00191
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                                                                                                                                                   11-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brownlee G, Choo KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1984-049331/08.
N-PSDB; AAN40142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 LVDRATCLR 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-1983;
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO8400560-A.
                                                                                                                                                                                                                                                                     diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP40222;
                                                                                                        AAP40178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP40222
ID AAP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                        RESULT 6
                                           AAP4017E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Factor-IX was used to construct recombinant adenovirus vectors that produced threspents levels of the clotring factor when administered to an animal host, potentially providing hemolilia B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                    The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine procease to natural substrates), esp. when admin. to give an intravascular blood concm. of 0.1-100 (pref. 0.5-10) microw. NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE.
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 46; DB 14; Length 415; Bet Local Similarity 100.0%; Pred. NO. 0.96; Matches 9; Conservative 0; Minantches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New adenoviral vectors for treatment of haemophilia - contg. DNA sequence encoding a clotting factor, partic. Factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watch 100.04; Score 46; DB 16; Length 454; Docal Similarity 100.04; Pred. No. 1.1, Conservative 0; Mismatches 0; Indels 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Factor-IX; blood-clotting; hemophilia B; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig. 11A-11B; 116pp; English.
Disclosure; Page 126-128; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67710 standard; Protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0218335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENETIC THERAPY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-US04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Connelly S, Kaleko M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-036495/05.
                                                                                                                                                                                                                    415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 330 LVDRATCLR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenovirus; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 LVDRATCLR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                      1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ76017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Factor-IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .0-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09429471-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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AAR67710;

RESULT 5 AAR67710

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Sequence

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Gaps

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Query Match

Best Loca Matches

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Lecocq JP;
                                                                                                                                                                                                                                                                                          the inventors claim a vector which comprises a DNA SQ coding for factor IX (FIX) and elements providing expression of this SQ in host calls. The prepn. of DNA FIX is as £0110-ws. Polyadenylared mRNA is 18018cd from humen lives, used to make ss-DNA which X1. St gressed with S1 and the fragments over 1 kD cloned in pRN 321. Clones are selected by Mystrdiamiton with a 52-mer probe corresp. to the bowine factor IX SQ (AAND0562).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The factor IX coding SQ (AANS0351) is first inserted into a non-
sesential region of viral DNA, cloned in a batterial plasmid. A
double-reciprocal recombination procedure is then used to transfer
the insert into the viral genome where it is propagated and
                                                                                                                                                                                   Cloning and expression vector for factor nine - for transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood clotting, haemophilia B; vaccinia vector; cowpox vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 46; DB 6; Length 461;
100.0%; Pred. No. 1.1;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tolstoshev P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vector for expressing factor 9 in vertebrate cells poxvirus genome in which factor 9 gene is inserted
                                                                                  Lecocq JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altenburger W,
                                                                                  Tolstoshev P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP50302 standard; Protein; 461 AA.
                                                                                                                                                                                                           bacteria, yeast or mammalian cells
                                                                                                                                                                                                                                                    Disclosure; Fig 3; 98pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 2; 59pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85WO-1104408.
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84FR-0007959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De La Salle H, Drillien R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of human factor IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                               De La Salle H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TRAN-) TRANSGENE SA.
(DSAL/) DE LA SALLE H.
                 (TRAN-) TRANSGENE SA.
(JAYE/) JAYE M.
                                                                                                                        WPI; 1985-302926/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1985-316884/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 LVDRATCLR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AANS0351
                                                                                                                                                N-PSDB; AANSO362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO8505376-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-1985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                               Jaye M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP50302
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 θĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim a recombinant DNA having a human factor IX sequence pref. at least 26 nucleotides long, esp. 75-7000 nucleotides. A cloning vector contg. foreign BNA is also claimed. The foreign sequence pref. includes the whole of an exon sequence of the foreign sequence pref. includes the whole of an exon sequence of the human factor IX genome. The cloning vehicle may be a modified comprising a DNA melacule having a single or double stranded probe sequence of is to 10000 nucleotides long factor IX DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of artificial human factor IX - by use of recombinant DNA sequences for host transformation and cultivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
100.0$; Score 46; DB 5; Length 456;
Best Local Similarity 100.0$; Pred. No. 1.1;
Matches 9; Conservative 0; Wismatches 0; Indels
              Haemophilia; Christmas disease; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human factor IX, encoded by DNA FIX.
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAPS0311 standard; Protein; 461 AA.
                                                                                                                        1..41
/label= signal
42..456
                                                                                                                                                                                                                                                                                                                                                                                                                   (NATR ) NATIONAL RES DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example, Fig 9; 49pp; English
                                                                                                                                                                                                                                                                                                                                83GB-0012490.
82GB-0022486.
83GB-0020975.
                                                                                                                                                                                                                                                                                          83GB-0020975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84WO-0007125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1984-057898/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 LVDRATCLR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN40177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brownlee GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1984;
                                                                                                                                                                                                                                                                                                                                   16-MAY-1983;
                                                                                                                                                                                                                                                                                          03-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1983;
                                                          Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8505125-A.
                                                                                                                                                                                                        GB2125409-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1985
                                                                                                                                                                                                                                                 07-MAR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP50311;
                                                                                                                                                      Protein
                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP5031
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Pactor X, factor IX, serine protease activity; catalytic domain, 2AD; 27mogen-activating domain; epidermal growth factor-like domain; EGF1; EGF2; regulator; cogquiation; fibrinolysis; homeostasis; X-ray structure; detection; drug modelling; restriction protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 46; DB 11; Length 461; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The slightly altered gene product has a higher ratio of PIX activity to FIX yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227..324
/label= catalytic domain
                                                             Factor IX; haemophilia B; vaccina; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA coding for human factor IX -
with mutation in pro coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW40284 standard; Protein; 461 AA.
                                                                                                                                             Location/Qualifier
                                                                                                                                                                  replace (44, Pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7..461
label= Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...46
label= signal
                    Mutant human factor IX (FIX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= EGF2
                                                                                                                                                                                                                                                                                                                     89EP-0403065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Factor IX protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.

Best Local Similarity 100.

Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; ; p; French.
                                                                                                                                                                                                                                                                                                                                                                                                       (TRAN-) TRANSGENE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-180758/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 LVDRATCLR 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LVDRATCLR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ05393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09747737-A1.
                                                                                                                                                                                                                                                                                                                     07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                              09-NOV-1988;
                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                            13-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meullien P;
                                                                                                                                                                                                                               EP373012-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW40284;
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AAW40284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The inventors claim vectors for expressing factor IX, or an analogous procein in vertebrate cells which consist of the genome poxylitus into which a gene coding for factor IX or an analogous procein has been inserted. Outlivation of infected cells produces very pure factor IX (a deficiency of which causes haemophilia B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector for expressing factor 9 in vertebrate cells - comprises
                                                                               Obery Match 100.0%; Score 46; DB 6; Length 461; Beet Local Similarity 100.0%; Pred. No. 1.1; Metches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilia B; blood clotting; factor IX.
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84FR-0007959.
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N-PSDB; AAN50049.
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                                         461 AA;
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expressed
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18-FEB-2000; 2000WO-EP01368.
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Matches 9; Conservative
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                                19-FEB-1999;
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                                                   19-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human feator IX processe. This procein is used in the construction of a noval non-glycosylated procein and truncated and symbol forms of this protein, which have settler procease activity. The procein is composed of various domains from a feator IX family procein. The procein is composed of various forms from a feator IX family procein. The procein is composed of various forms of the procein and procein from a feator IX family proceins of the procein forms of the procein from the procein in ZDD, which incomes feator IX family proceins (posterially useful as required to consider the procein in zymogen form is also useful. In assays for descripting factor IX and scrivity in equence solution (specifically in bod description). The procein in zymogen form is also useful as the procein in zymogen form is also useful as with proceins of an inhibitors for X-ray structural analysis and drug modelling and a brestition prices or inhibitors for X-ray structural analysis and drug modelling where has an especificative as factor IX family processes and ensure forms and ensure cleaves and can be vorticed to an adversarial and an analysis and an analysis and an analysis of the same specificative as factor IX family processes and can be restricted by the processes and can be restricted by the processes and can be restricted by the processes and can be surfaced by the surfaced by the processes and can be surfaced by the processes and can be surfaced by the processes and can be surfaced by the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                     Non-glycosylated, truncated forms of factor IX family protein with serine protease activity - used to screen for specific modulators and to assay factor IXa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant DNA; gene therapy; hormone responsive element; transgene; HRB; heamophila; clotting factor IX; vaccine; regulation; breast cancer; ovarian cancer; prostate cancer; you Willebrand disease; cystic fibrosis; hormone; receptor; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 46; DB 19; Length 461; 100.0%; Pred. No. 1.1;
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                                                                                                                                                    (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 4; 49pp; German.
                                                 97WO-EP03027
                                                                                  96EP-0110959
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                                                                                                     96EP-0109288
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Matches 9; Conservative
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                                                                                                                                                                                       Hopfner K, Kopetzki E;
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                                                 11-JUN-1997;
                                                                                                                   22-JUN-1996;
                                                                                06-JUL-1996;
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                18-DEC-1997.
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X2X5X8X55555XXX2X8X
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The would be allowed the standagene (T). Alternatively the muleic acid constitute, comprises at least one HRE and a transgene where one of the HREs is not functionally linked to the transgene, where one of the HREs is not functionally linked to the transgene, where one of the HREs is not functionally linked to the transgene, or the constructs can be used to up-regulate to rdown-regulate transgene, the constructs preferably comprise a transgene which encodes a protein which is lacking in a variety of general cisorders or involved in conditions related in inappropriate responses to hormones, for example hormone-dependent cancer. The transgene may also be used to replace a defective gene cancer. The transgene has also be used to replace a defective gene cancer. The transgene has also be used to replace a defective gene cancer. The transgene has hamen clotting account to an organism or to a cellular system. The constructs have applications in gene therapy for transfere. The organism or to a cellular system. The constructs have applications in gene therapy for transfere may be constructed advantage of this system is that the hormone-teceptor complex contains a hormone receptor that becomes activated after binding off its appecific hormone. The hormone receptor in the activated state is also also also and a hormone receptor that becomes activated after binding off the preconsile.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid constructs are described which comprise an hormone
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                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid construct useful in gene therapy comprising an normone responsive element and transgene in which the hormone responsive element is not functionally linked to the transgene
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Mismatches . 0; Indels
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(THER-) THERAGENE BIOMEDICAL LAB GMBH.
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The invention relates to unitates and sequences which regulate game expression in an age-related manner and/or in a livering regulatory sequences are regions of the human factor. If hirty game, and regulatory sequences regions of the human factor. If hirty game, and regulatory sequences are equal to the first age-related regulatory sequences are designated ABS' (AFF6016) and ABS' (AFF6017) and are found in the 5' CT UTR (at position 1264-1265 of AFF6016) are appectively. These alements act synergistically conformed hirty levels over the lifespan of an individual, however, they can independently exert effects on hirty and an individual, however, they can independently exert effects on hirty and an individual, however, they can independently exert effects on hirty and an individual, however, they can independently exert effects on hirty and an individual, however, they can independently exert effects on hirty and an individual, however, they can independently exert effects on hirty and an individual, however, they can independently and contains two PBA-3 (bolyona virus activator 3) elements (AFF60013), and contains two PBA-3 (bolyona virus activator 3) elements of the invention, along with their homelogues, variants and fragments may be used in the construction of recombinant expression vectors include those encoding proceins involved in blood conjulation (e.g., the pro-ocepulante factor x premeter, the Ty promoter. The analysis of the construction of the construc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis cardiovascular disease, diabetes Alzheimer's disease, parkninnes disease, cardiovascular disease, carcer, oseeopoosas, ostecanthricis and demental specifically, they may be used to express factor ix antisense mRNA in the treatment of thrombotic conditions associated with the natural age-related rish in factor IX expression. Transgenic cells or animals that contain vectors of the invention are useful as models of these diseases, in acreening for potential therapeutic agents and for suidals normal processes such as againg and gene expression. Frequents and homologues of age-related regulatory sequences, are useful as probes to detect, isolate or identify other such sequences in samples. The present
                                                                                                                           The invention relates to nucleic acid sequences which regulate gene
            New regulatory elements that control age-related gene expression, useful in gene therapy and for reducing Factor IX expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
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                                                                                Disclosure, Fig 8A-E; 225pp; English.
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Job time: 42.95 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to an improved method for the production of recombinant human blood clotting factors, especially factors VIII and IX. Weing an immortalised cell line stably expressing viral transcription activators and carrying a vector comprising a promoter and a sequence encoding the blood coaquilation factor. The factor VIII mutein or a gene transfer vector is used in the preparation of agents for treating hamonalila, especially hamonabilia a. The present agence is human wild-type factor IX protein snooded by vector for professing.
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                                                                                                                                                                                                                                                                                                                                                Recombinantly producing human blood coagulation factors VIII and IX for use in treating hemophilia -
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                                                                                                                                                                                                                                       Schroeder C, Lehnerer M;
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                                                                             21-MAR-2001; 2001WO-EP03220.
                                                                                                                        22-MAR-2000; 2000EP-0106225.
08-MAY-2000; 2000US-203249P.
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Best Local Similarity 100.
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                                                                                                                                                                                         (OCTA-) OCTAGENE GMBH
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N-PSDB; AAF54018.
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                                     27-SEP-2001.
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OM protein - protein search, using sw model

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US-09-851-422B-2 20 1 DRAT 4 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp_codent:*
sp_vinus:*
sp_vinus:*
sp_unclassified:*
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sp_vacteriap:*
sp_acteriap:* SPTREMBL_21:*

1: pp_arches:*

2: pp_bacteria:*

3: pp_tungi:*

4: sp_tungi:*

5: sp_invertebrate:*

6: sp_manmal:*

7: sp_mm:* sp_organelle:* sp_phage:* sp plant: *

Pred. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query	ŗ				
Matc	÷	Match Length DB	DB	ID	Description
100	. 0	25	101	P82952	P82952 prunus dulc
100	0	27	12	091KR6	Ogikre hepatitis c
100	0	31	ч	08X254	O8x254 halobacteri
100.0	-	45	e	Q9URG8	Oguras rhizomucor
100.0		46	N	098604	Q98604 escherichia
100.0		48	16	Q8XXT7	Q8xxt7 ralstonia s
100.0		49	10	Q9LJS3	O9lis3 arabidopsis
100.0		53	13	Q90XF3	090xf3 coturnix co
100.0		9	'n	090415	Q9u415 tetrahymena
100.0		63	12	Q65240	Q65240 african swi
100.0		63	17	Q9HQ75	Q9hq75 halobacteri
100.0		64	σ	Q9AYU9	Q9ayu9 lactococcus
100	_	64	10	QBW0J3	O8w013 oryza sativ
100	0	64	16	Q9CFP1	Ogcfpl lactococcus
100	0	99	4	9NIN6O	Ogntn6 homo sapien
100	0	67	16	091607	O916n7 salmonella

Q8x3y5 escherichia Q9x3y5 escherichia Q9121; atreptomyce Q9121; bomo sapien Q91R8 homo sapien Q99R82 thizoblum 1 Q99R92 thizoblum 1 Q99R92 thizoblum 1	VADOJA MAYOZACCET Q9h122 thermoplasm Q9pd28 xylella fas Q8xw88 tabsconia s Q06656 streptomyce Q36656 thuman astro	O9kdl8 bacillus ha 088153 rhizobium e 086518 homo sapien 08v293 arabidopsis 08sb16 oryza sativ	Q8tb11 homo sapien Q8ty18 streptomyce Q88076 oryza sativ Q86819 human astro Q9aupl oryza sativ Q9406 drosophila	Obyky3 anabaena sp Q01667 heparitis c Q3833 lactococcus Q64186 cavia (guin Q98444 rhizobium l
16 Q8X3YS 16 Q9L2J1 4 Q9NUS8 4 Q9NR86 16 Q98P82 16 Q98P82	7 250524 16 09PD28 16 08XW88 2 006656 12 039862	16 Q9KDH8 2 Q88153 4 Q96JR8 110 Q8VZ93 11 Q48E16	4 Q8TB31 16 Q9KY18 10 Q8S076 12 Q96819 10 Q9AUP1 5 Q9V4G6	16 0984W4
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25 AA.	01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	01-10N-2001 (TrEMBLrel. 17, Last annotatio Seed allergenic protein (Fragment). Trunus dulcis (Almond) (Prunus amygdalus).	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;	eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.				z	"Identification of IgE-binding proteins as 28 albumin and conglutin in		Submitted (FEB-2001) to the SWISS-PROT data bank.	-!- FUNCTION: MAY FUNCTION AS SEED STORAGE PROTBINS. HAS AN IGE-				RING	Allergen, IgE-binding protein; Seed storage protein.		25 AA; 2872 MW; A04173DC65B48C99 CRC64;
,-	ed) sequ	anno .). iygda	phyt	iygda				hmae	otei		- PRO	D ST		SUBCELLULAR LOCATION: CYTOPLASMIC.		00 01	ed B		7300
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	(TrEMBLrel. 17, Created)	01-JUN-2001 (TEMBLEEL. 17, LABE AF Seed allergenic protein (Fragment). Prunus dulcis (Almond) (Prunus amyo	, St.	acea			SEQUENCE.	X.	indi	almond (Prunus dulcis) seed.";	the	ON A		5	SEED	EXP	otei		W.
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Ouery Match 100.0%; Score 20; DB 10; Length 25; Bet Local Similarity 100.0%; Pred. No. 89; Matches 4; Conservative 0; Mismatches 0; Indels

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RESULT 2

27 AA

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Hepatitis C virus

SEQUENCE PROM N.A. NCBI_TaxID=11103;

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BUDNINE-92242013; PubMed=10227474;
Reingold d., Sterr N., Maurer J., Lee M.D.;
Reingold d., Sterr N., Maurer J., Lee M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE-92105011, PubMeda-1729337,
DISanto M.E., Li O.H., Logan D.A.;
Pourification and characterization of a developmentally regulated
extroxypepticates from Mucor tracenosus.";
J. Bacteriol. 174:447-455 (1992).
                                                                                                                                                          01-JUN-2001 (TrEMBLrel: 17, Last annotation update)
Carboxypeptidades 3, CP3 (Fragments).
Rhizomucor revenosus (Nucor circinelloides f. lusitanicus).
Eukaryota; Pungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae,
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Escherichia.
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                                                                                                                                    , Last sequence update)
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Vet. Microbiol. 66:125-134(1999).
EMBL, AF052225; AAD28082.1; -.
NON TER 46
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01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein RSC2026.
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                                      PRELIMINARY;
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Bidde K.A.;
"Differential expression of genes influenced by changing salinity
using RNA arbitrarily primed PCR in the archaeal halophile, Haloferax
                                                                                              Occr-2000 (TrEMBLeal. 15, Created)
01-CGT-2000 (TrEMBLeal. 15, Last sequence update)
01-DEC-2001 (TrEMBLeal. 15, Last annotation update)
01-DEC-2001 (TrEMBLeal. 19, Last annotation update)
(MSIJ) (Freagment) (Ontains: envelope glycoprotein E2 (GP68) (GP70)
(MSIJ) (Freagment).
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InterPror, TRN050531, HCV, NS1.
Pfam, PP051560, HCV, NS1.
Pcode protein; BrNe10pe protein; Glycoprotein; Nonstructural protein; Pcolyprotein; Transmembrane.
NON TER.
NON_TER.
SEQUENCE 27 AA, 2768 MM; 2P457A89D77D2263 CRC64;
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Hapacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus replication and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                izoper J., Rostaing L., Sandres K., Cisterne J.M., Pasquier C., Rumeau J.L., Duffaut w., Durand D., Poul J., Pull J., Pull J., Longon J., Poul J., 
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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01-MAX-2002 (TrEMBLEA). 20, Last sequence update)
01-MAX-2002 (TrEMBLEA). 20, Last sequence update)
01-MAX-2003 (TrEMBLEA). 3.6 km sprotein (TreMBLEA). 3.6 km sprotein (TreMBLEA). 3.6 km shortering update)
Halobacterium volcanii (Halobacteria). Halobacteriales;
Halobacteriaceae, Halofacax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 27
27 AA; 2768 MW; 2F457A89D77D2263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 31 AA; 3609 MW; 682119419273C9D0 CRC64;
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0; Mismatches

ilarity 100.0%; Conservative 0

Local Similarity

Best Loc Matches

Query Match

10 DRAT 13

1 DRAT 4

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PRELIMINARY;

Q8X254 Q8X254;

RESULT 3

08X254

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Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                         27 DRAT 30
                                           . 1 DRAT 4
                                                               8
                                             ઠે
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RESULT 4 .

100.04;

EMBL; AF454092; AAL57845.1; Hypothetical protein.

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Enkaryova, Alveolata, Cillophora, Oligohymenophorea, Hymenostomatida, Tertahymenina, Tetrahymena. Neil Taxahymena.
                                                                                                                                        Coturnix coturnix (common quail).
Bukaryota; Wetazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Archosauria; Avesi Neoganthae, Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                               EQUINCE FROM W. Schneider M.L., Bister K., Hartl M.;
Bader A.G., Schneider M.L., Bister K., Hartl M.;
"1003, a target of the v-Jun transcription factor, encodes a protein with transforming activity related to human microspherule protein 1 (MCRS1)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 13; Length 53; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang H., Huang X., Berger J.D.,
R. QcLin.like sequence in Tercathymena thermophila.";
R. QcLin.like sequence in Tercathymena thermophila.";
L. ShulthaRir: BELONGS TO THE CYCLIN FAMILY.
HEBR: PRICAZZO; ARTISE4.1;
HEBR: PRO134: QCLIN.
FRAN; PRO134: QCLIN.
FRAN; REFOLISS: CYCLIN.
PRONITE: PRO135: CYCLIN.;
ROSITE: PRO135: CYCLIN.;
ROSITE: PRO135: CYCLIN.;
ROSITE: PRO135: CYCLINS;
ROSITE: PRO135: CYCLINS;
ROSITE: PRO14: GCLINS;
ROSITE: PRO14: GCLINS;
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ROSITE: PROMITER TO THE TERCATE THE THE TERCATE T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
6325 MW; 325C0B53BE2F8D27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AA; 7020 MW; 803EC056F39D45D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                  (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitotic cyclin-like protein (Fragment)
                                                                                                      Myosin-binding protein H (Fragment).
    01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 0:0-0(2001).
EMBL; AF390035; AAK73733.1; -.
NON TER 1 1
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(TrEMBLrel. 13, I
(TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetrahymena thermophila.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 AA;
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                                                                                                                                                                                                                                                                           NCBI_TaxID=9091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CU427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 DRAT 38
                             01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRAT 4
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01-DEC-2001
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SEQUENCE
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Q65240
ID Q65240
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"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4.251,695 bp covered by ninety P1,
PMC and BC 17.221 (2000)
BMB. Res 7.217-221 (2000)
BMB. Res 7.817-281 (2000)
BMB. A POOR 11: PARATA 1: 5.572 WH; 5.2A72 M47F98D5126 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bikaryota : Viridiplantae; Straptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; errosida Ili Bassicales; Brassicaces; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                   Artisoundar M. Genin S. Artisonaive P., Goury J., Mangenoc S., Artis M. Billauth A. Brottiar P Camus J.C., Cattolico L., Cattolico L., Chandler Billauth R. Brottiar P Camus J.C., Cattolico L., Demander M., Claudel-Renard C., Cumac S., Demange N., Espainer M., Chandler M., Chinar A., Robert C., Sautin M., Schiax F., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Schiax F., Genome Bequence of the plant pathogen Raletonia solanacearum."; Watter 415:49-2021202).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-COLUMBIA;
Kaineko T. Kato T. Sato S. Makamura Y. Asamizu E., Tabata S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databasee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                             Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score'20; DB 10; Length 49; 100.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 16; Length 48; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 48 AA; 5473 MW; 66CDA3D6402F3718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-007-2000 (T-EMBLrel. 15, Last sequence update)
01.007-2000 (TFEMBLRel. 15, Last sequence update)
01.007-2001 (TFEMBLRel. 19, Last sequence update)
6cenate on Mr. chromosome 3 TM Colone: ALIL114.
Arabidopsis chailana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%; Pred. No. 1.8
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                    STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4, Conserv
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RSC2026 OR RS03598
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Q90XF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LJS3
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OUTUNES FROM N.A. SECULO Lectis bacteriophage Tuc2009; SPECIES—Lactococcus Lectis bacteriophage Tuc2009; SPECIES—Lactococcus Ly. van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.; Van Sinderen D., van de Guchte M., Seegers J. account plage Tuc2009; ", Nobecliar analysis of the temperate Lactococcus, plage Tuc2009; ", Submitted (FBB-2000) to the EMBL/GenBank/DBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIAS-Hange bil285, and Phage bil286;
MEDLINE-21113149; Dubmed-11160885;
MEDLINE-21113149; Dubmed-11160885;
MEDLINE-21113149; Dubmed-11160885;
MEDLINE-21113149; Dubmed-1160885;
MEDLINE-2111403; Gifferent generic structure of temperate and virulent phage populations.";
Nucleac Acids Ress. 29:644-651(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyra, Embryophyta, Tracheophyta, Sprantophyta, Magnoliophyra, Liliopaida, Poales, Poaceae;
Shrhartoldae, Oryzaea; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                          stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-Phage bill36, and Phage bill286;
Chopin A. Bolotin A. Gorokin A. Ehillch S.D., Chopin M.-C.;
Submitted (NOV-2000) to the BHBL/GenBank/DDBJ databases.
BHBL; AF108674; ANX19849.1; --
BHBL; AF218669 AAX08234.1; --
BHJCHELTAB protein.
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SasakX T., Wartsumoto T., Yamamoto K.;
"Ofyza atiya nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 9; Length 64; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone.P0007F06.".
Submitted (FRB-2010) to the EMBL/GenBank/DDBJ databases
EMBL, AP003223; BAB84370.1; -...
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                            64 AA
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                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis bacteriophage Tuc2009
                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Leat seq
01-DEC-2001 (TrEMBLrel. 19, Leat seq
Hypothetical 7.6 KDa protein (Orf9).
ORF9.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA st
NCBI_TaxID=35241, 151535, 151536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20,
20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
hes 4; Conservative
                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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47 DRAT 50
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01-JUN-2001
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                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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EMBL; AE005052; ANG19642.1;
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STRAIN-MAIANT LILEO /1;
Dixon L.K., Twigg S.R.P., Baylis S.A., Wydelingum S., Bristow C.,
Hammond J.M., Smith G.L.
Nucleacide sequence of a. 55 kbp region from the right end of the
genome of a pathogenic African swine fever virus isolate (Malawi.
                                                                                                                                                                                                                                                             STRAIN-WALAWI LILOO /1, WEDLINE-WALAWI LILOO /1, WEDLINE-SALAHI LILOO /1, WEDLINE-SALAHSSE, DUADE-8409937, WEDLINE-SALAHSSE, DAYLIS S.A., BAYLIS S.A., BAYLIS S.A., BAYLIS S.A., "Duplicated genes within the variable right end of the genome of pathogenic lisolate of African swine fever virus."; J. Gen. Virol. 74:2125-2130(1999).
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                                                                                       ORF jist.
Akrican swine fever virus (ASFV)
Viruses, debna viruses, no RNA stage; Asfarviridae; Asfivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 63;
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Arabbaccerium ap. (strain NRC-1).
Archaea, Euryarchaecta; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. GEN., Virol. 7:1655-1684 (1994).
EMBL; X71982; CAASO816.1; -.
SEQUENCE 63 AA; 6851 MM; 7C1AC866CDDP4EEB CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annocation update)
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01-WAR-2001 (TrEMBLrel. 16, Late sequence update)
01-WAR-2001 (TrEMBLrel. 16, Late annotation update)
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE 63 AA;
                                                                                                                                                                          NCBI TaxID=10497,
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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36 DRAT 39
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Q9HQ75,
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RESULT 11 **09HQ75**

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Gaps

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EMBL; AD006373; AAK05524.1;
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis (subsp. lactis) (Streptococcus lactis), sateris, Pirmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcacaes Lactococcus, NCBL TaxID=1160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo appiens (Human)
Bukaryosa, Merzaosa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalais, Butheria, Primares, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                        h 100.0%; Score 20; DB 10; Length 64; Similarity 100.0%; Pred. No. 2.5e+02; 4; Conservative 0; Mismatches 0; Indels
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NOW_TER 6 6 6 SE
SEQUENCE 66 AA; 7022 MW; 218B520004B6E6AA CRC64;
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SEQUENCE 64 AA; 7573 MW; 740DC4287228266F CRC64;
64 AA; 7286 MW; 21256P1F01116535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Laff Sequence update)
01-JUN-2002 (TrEMBLrel. 20, Lagt annotation update)
Prophage 913 protein 53.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last anhotation update)
BB94P8.1 (KIAA1326) (Fragment).
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MEDLINE=21235186; PubMed=11337471;
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                                                                        Query Match
Best Local Similarity
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SEQUENCE
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US-09-851-422B-2 20 1 DRAT 4 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ption	escherichia	thermus the	vaccinia vi	tityus bahi	tityus serr	tityus stig	rhizobium e	schizosacch	mycobacteri	orgyia pseu	neisseria m	neisseria m	synechococc	rhizobium s	zea mays (m	equus cabal	haemophilus	buchnera ap	gallus gall	escherichia	escherichia	вупеснососс	mycobacteri	ureaplasma	streptomyce	streptomyce	escherichia	salmonella	halobacteri	rhodococcus	homo sapien	mus musculu	rattus norv
Description	P39166	P43891	P20526	P56611	P15226	P56612	P24901	009730	P50048	010307	09 jw46	09jxs6	006865	P55396	041764	P06714	P43758	P57294	068060	P41443	P23484	055024	053717	09pqh6	P40178	Q9x8r7	P26427	P19479	P13076	P20771	014807	008989	P97538
8	YIFL ECOLI	PYRH THETH	YVAQ VACCC	SCX7_TITBA	SCX7_TITSE	SCX7_TITST	ACPA_RHIET	YA4D_SCHPO				RNPA NEIMB	AMPA SYNP7	TRBC_RHISN	ADF3_MAIZE	HBAT HORSE		DKSA BUCAI		GSPH_ECOLI	FECI_ECOLI	DPSA SYNP7	PYRE_MYCTU	IPYR_UREPA	PURS STRFR		AHPC_ECOLI			YNHA_RHOER		RASM_MOUSE	RASM RAT
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* Query Match Length	67	70	77	84	84	84	16	91	104	109	121	121	125	127	139	141	145	151	160	169	173	176	179	181	182	182	186	186	193	199	208	208	208
Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	20	50	20	20	20	20	20	20	50	20	50	20	20	20	20	20	20	20	20	20	20	20	20	50	20	50	20	50	50	20	20	50	20
Result No.	-	7	Э	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	53	30	31	32	33

P09879 streptococc	Q52081 pseudomonas	P16038 ovis aries	O66929 aquifex aeo	031749 bacillus su	Q05613 pseudomonas	P00746 homo sapien	P71693 mycobacteri	P22866 streptomyce	Q00813 haloarcula	P74457 synechocyst	Q9cka5 pasteurella
PROB STRAG	FLGH PSEPU	PLL SHEEP	PYRH AQUAE	PYRH BACSU	TONB PSEPU	CFAD HUMAN	YE24 MYCTU	GYLR STRGR	RPOD HALMA	PYRH SYNY3	YH20_PASMU
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226	231	236	240	240	243	253	253	254	259	260	260
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34	35	36	37	38	39	40	41	42	43	44	45

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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2010 (Rel. 40, Last amocation update)
16-OCT-2010 (Rel. 40, Last amocation update)
Toxin gamma precursor.
Titytus bahisnals (Brzallian scorpion).
Buthoidea; Buthidae; Tityus.
(CII _TAXID=50343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Appendix to 'The complete DNA sequence of vaccinia virus'."; Virology 179:517-563(1990).
                                                                        100.0%; Score 20; DB 1; Length 70; 100.0%; Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 1; Length 77; 100.0%; Pred. No. 57; ive 0; Mismatches 0; Indels
                                                                                                                                                       Indels
     7B8AB85DDA977CEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 AA; 8635 MW; 12BBC61FF7472771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Created)
16-0CF-2001 (Rel. 14, Lest sequence update)
16-0CT-2001 (Rel. 40, Lest amotation update)
A ORF Q.
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                                                                                                                  Local Similarity 100.0%; Pred. No. 52, tes 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91021027; PubMed=2219722;
     70 AA; 7629 MW;
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Hypothetical protein
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NCBI_TaxID=10249;
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P20526;
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     SEQUENCE
                                                                              Query Match
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Bachgation factor Te from Thermus thermophilus -- overproduction in sachertchia coli, quaternary tenemes thermophilus -- overproduction in a colingation factor Tu.;
Bur. J. Blochem. 236:222-227(1996).
-- FUNCTION: URIDIUS MONOPHORPHATE KINASE (BY SIMILARITY).
-- CATALYTIC ACTIVITY: A THP - UUP = ADP + UUP = ADP + UUP - CATALYTIC ACTIVITY: ATP + UUP = ADP + UUP - ADP +
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SIMILARITY: TO OTHER UMP KINASE; SOME, TO ASPARTOKINASES AND TO
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01-NOV-1995 (Rel. 32, Last sequence update)
30-MNY-2000 (Rel. 33, Last annotation update)
Uridylate kinase (RC 2.7.4.-) (UK) (Uridine monophosphate kinase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 67 DGPSQVNY -> MVHPR (IN REF. 2)
67 AA; 7177 MW; 4A52CP48A555A7F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20, DB 1; Length 67; 100.0%; Pred. No. 50; ive 0; Mismatches 0; Indels
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Pfam; PR00696; aakinase; 1.
Trangfarase; Kinase; Pyrimidine biosynthesis.
NON TER 70 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
CONFLICT 60 67 DGPSOVNY ->
SEQUENCE 67 AA; 7177 MW; 4A52CP48A555
Nucleic Acids Res. 22:4756-4767(1994).
                                                                                                                                                                                                                                                                                                                                                                  EMBL, M87049; -; NOT_ANNOTATED_CDS.
EMBL, AE000457; -; NOT_ANNOTATED_CDS.
EMBL, XE6792; -; NOT_ANNOTATED_CDS.
EMBL, AE01542; -AAG$001.1; -.
EMBL, AP015567; -, NOT_ANNOTATED_CDS.
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MEDLINE=96184901; PubMed=8617268;
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Matches 4; Conservative
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NCBI TaxID=274;
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PYRH_THETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possani L.D., Martin B.M., Mochca-Morales J., Svendsen I.; Possani L.D., and chemical characterization of the major toxins from the venom of the brazilian scorpion Titus serrulatus Lutz and Mello."; Carleberg Res. Commun. 46:155-205 [1991].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                              Possani L.D., Martin B.M., Fletcher M.D., Fletcher P.L. Jr.; wishedaage effect on pancreatic exocrine secretion produced by toxins purified from Tityus serrulatus scorpion venom."; J. Blol. (Amm. 266:31P8-3185(1991).
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                        MEDLINE=64307524; PubMed=6477555;
Bechis G., Sampieri F., Yuan P.-M., Brando T., Martin M.-F.,
Diniz C.S., Rochat H.;
'Amino acid sequence of toxin VII, a beta-toxin from the venom of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATIONALITY.
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AMIDATION (G-82 PROVIDE AMIDE GROUP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sampaio S.V., Arantes E.C., Prado W.A., Riccioppo Neto F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurotoxin; Sodium channel inhibitor; Amidation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430F3FCA74823E77 CRC64;
                                                                                                                                scorpion Tityus serrulatus.";
Biochem. Biophys. Res. Commun. 122:1146-1153(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00537; toxin_3; 1.
ProDom; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92023285; PubMed=1926167;
                                                                                                                                                                                                                                                            MEDLINE=91131623; PubMed=1993690;
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Similarity 100.0%;
4; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X66256; CAA46982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S66941; AAB29128.1; -.
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PIR; S21158; S21158.
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                                                                                                                                                                                                           SEQUENCE OF 21-81.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-62.
                                                                                                                                                                                                                                TISSUE=Venom;
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MOD RES
SEQUENCE
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                                                                       Bacerrif B., Corona M., Coronas F.I., Zamudio, F. Colderon-Arada E.S. Fletcher P. L. Tr. Martin B.M., Possani L.D.; "Toxic peptides and genes encoding toxin gamma of the Brazilian "Toxic peptides and genes encoding toxin gamma of the Brazilian Brochen 311919-760(1996). "Bit This Arada S. T. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin-Eauclaire M.-F., Ceard B., Ribeiro A.M., Diniz C.R., Rochat H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1993 (Rel. 26, Last sequence update)
01-UUL-1993 (Rel. 41, Last sequence update)
10-UUL-2002 (Rel. 41, Last annotation update)
10-UNL-2002 (Rel. 41, Last annotation update)
11-UN (TOXAN III.10) (TOXAN Gamaha) (TOXAN T2-IV)
11-UN (TOXAN III.10) (TOXAN Gamaha) (TOXAN T2-IV).
11-UVB SETULATURE (BRAZILIAN SCOTPION).
12-UN (MARZOR) ARTHNODOMA; Chelicerata, Arachnida, Scorpiones)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possani L.D.; "The genomic region encoding toxin gamma from the scorpion Tityus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-82 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and nucleotide sequence analysis of a cDNA
encoding the main beta neurotoxin from the venom of the South
American scorpion Tityus serrulatus";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotoxin; Sodium channel inhibitor; Amidation; Signal.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB
Pred. No. 63;
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SEQUENCE FROM N.A., AND SEQUENCE OF 21-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOXIN GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROBABLE)
                                                                                                                                                                                                                                                                                                    RSBFA-TOXN USURPANILY.
ILICEPPO 1 PRODUCT, Knot 1
ILICEPPO 1 IRRODGEL, Knot 1
ILICEPPO 1 IRRODGEL, Scorphon_LoxinL.
PRODOM: PRODGEN, COXID. 3, 1
PRODOM: PRODGEN SCORPION_LOXIDL, 1.
PRODOM: PRODGEN SCORPION_LOXIDL, 1.
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                                              WEDLINE=96190713; PubMed=8611151;
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FEBS Lett. 335:6-8(1993).
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larity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buthoidea; Buthidae; Tityus.
NCBI_TaxID=6897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9384 MW;
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INIT MET
BINDING
SEQUENCE
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       Soberon
 ö
                                                         Toxin gamma precursor.
Tityus stigmurus (Brazilian scorpion).
Makaryota, Metazoa Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoides; Buthidee; Tityus.
                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-82 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium leguminosarum (biovar viciae).
Becteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
Rhizobiaceae, Rhizobium.
NCBL_Tax1D=29449, 387;
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                          Score 20; DB 1; Length 84; Pred. No. 63; 0; Mismatches 0; Indels
                                                                                                                                                                                                                     Neurotoxin; Sodium channel inhibitor; Amidation; Signal
                                                                                                                                                                                                                                                                            460653ABAE1F7877 CRC64;
                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 20-81 FROM N.A.
                                                15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            ACPA_RHIET STANDARD; PRT; 91 AA. P8401, 08813; 01-ARA-1922 (Rel. 21, Created) 15-UNK-2002 (Rel. 41, Last sequence update) 15-UNW-2002 (Rel. 41, Last semotation update) Acyl carrier protein acpXL (ORF*).
                                                                                                                                                                                                                                   TOXIN GAMMA.
                                                                                                                                                                                                                                                                       (PROBABLE)
                               PRT;
                                                                                                              WEDLINE=96190713; PubMed=8611151;
                                           (Rel. 37, Created)
                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                             9366 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=R.etli; STRAIN=CE3;
PubMed=11717256;
                                                                                                                                                                                                                                                                                                     Conservative
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium etli, and
                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                             84 AA;
                                                                                                        IISSUE=Venom
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                                          5-DEC-1998
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                             SCX7 TITST
P56612;
75 DRAT
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MOD_RES
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                        SCX7_TITST
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                  RESULT 6
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MOI. Gen. Genet. 223:138-147(1990).

1. FURCTOR: Carrier of the growing fatty acid chain in fatty acid constructions carrier of the growing fatty acid chain in fatty acid for the fatty acid is involved in the transfer of long hydroxylated fatty acids to lightd A. Is acylated predominantly with 27-fatty acids to lapid A. Is acylated predominantly with 27-fatty acids to blogonhuse in a construction of the lapid A. Is acylated predominantly with 27-fatty lapid A blogonhuse is transferred from CoA to a specific construction by acys. This modification is essential for acid, acid, the proathetic group.

1. Subcardowerry: Wwwloafs or WETHOD-Electrospray; RANGE-Isoform construction with 4 "phosphopanetheline."

2. SHMIAMITY: COTRAINS 1 ACTL CARRER DOWAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE RROW N.A.
SPECIESA.1 vicines.
Basu S.S., Kabarz M.J., Raetz C.R.H.;
Basu S.S., Kabarz M.J., Raetz C.R.H.;
Tappession cloning and characterization of the C28 acyltransferase of Third A blosynthesis in Rhizoblum leguminosarum lipid A N.Y.
incoporation into Rhizoblum leguminosarum lipid A N.Y.
submitted (MAY-2002) to the BMBL/GenBank/DB03 databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=R.1, viciae; STRAIN-VF79;
MEDLINE=210806954; PubMed=2175385;
Colonna-Romano S., Arnold W., Schlueter A., Boistard P., Puehler A.,
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SEQUENCE OF 1-27, 29-40 AND 68-74, CREARCTERIZATION, AND MASS SPECTROMETRY.

GREARCTERIZATION, AND MASS SPECTROMETRY.

GREARCTERIZATION, AND MASS SPECTROMETRY.

BECLINE-97113013 Pubmed-8943266.

BECLINE-97113013 Pubmed-8943266.

BECLINE-87113013 Pubmed-8943266.

"A special acyl carrier protein for transferring long hydroxylated fatty acids to lipid A in Rhizobium.";

Solo. Tome. 271130126-23136(1996).
                                                                                                 etli: role of FnrN in EixNoOP expression and in symbiotic nitrogen fixation.";
                                                                                           'Regulation of gene expression in response to oxygen in Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PP00550; pp-binding; 1.
Procom; PD00689; A27, Carrier; PP00689; A27, Carrier; PP0051EP; PS00012; PH05EP00PMTETHEINE; 1.
PR05ITE; PS00015; ACP DOWAIN; 1.
Lipid synthesis; Lipid A biosynthesis; Patty acid biosynthesis; Phospingancetheine.
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on M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8E2E71DBAAB7B5A3 CRC64;
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EMBL, AF510733; AAM44294.1; ALT INIT.
EMBL, X55788; CAA39311.1; ALT_INIT.
PIR; S11950; S11950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003231; Acyl carrier.
InterPro; IPR003880; Ppantne_attach.
                                                                                                                                                                                                                    J. Bacteriol. 183:6999-7006(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF083916; AAC34462.1; -.
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100.0%; Score 20; DB 1; Length 91;

104 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITARS-982999; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Badcock K., Bagham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Bagham D., Brown D., Chillingworth T., Connor R.,
Barloney T., Jagels K., Krogh A., McLean J., Moule S., Hemlin N., Holroyd S.,
Bornier S., Geborne J., Quall M.A., Raplandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Complete genome sequence.",
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,
Rolonay J.F., Nelson W.C., Daylam L.A., Ermolaeva M.D., Salbree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96032403; PubMed=7559354;
Clemens D.L. Lee B.Y., Howktz M.A.;
"Purification, characterization, and genetic analysis of
Mycobacterium tuberculosis urease, a potentially critical determinant
of host-pathogen interaction.";
O' Bacteriol. 177:664-6622(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE=96004620; PubMed=7568014; MEDIJNE=96004620; PubMed=7568014; MEDIJNE=96004620; PubMed=7568014; MEDIJNE=960040 of Mycobacterium tuberculosis and its utilization for the demonstration of allelic exchange in Mycobacterium bovis bacillus Calmette-Greenin, 1, 82.8, 92:8768-8772 (1995).
                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium;
NCBI_TRACIB-1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases.
-- CATALYITC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3)
-- SUBDIT: (ALBHA, BETA, GANMA) (3) (BY SHIMLARITY)
-- SUBDIT: (ALBHA, BETA GANMA) (2)
                                                                                                                                                        01-007-1996 (Rel. 34, Created)
10-007-1996 (Rel. 34, Last sequence update)
16-007-2010 (Rel. 40, Last amoration update)
16-007-2010 (Rel. 40, Last amoration update)
URBER PRINGES (E. 3.5.1.2) (Urea amidohydrolase)
URBER RY1849 OR MY1897 OR MYCX395.24C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 393:537-544(1998).
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                       URE2 MYCTU
P50048;
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                                                                                 JRE2 MYCTU
                                                                                                                                     MEDINES-1888019 PubMed=11859360,
MEDINES-1888010 PubMed=11859360,
MEDINES-1888010 PubMed=11859360,
MEDINES-1888010 PubMed=11859360,
MEDINES-1888010 PubMed=11859360,
MEDINES K. Brown D., Barden S., Basham D., Bowman S.,
A. Gollis M., Comor R., Croinin A., Davis P., Feltwell T., Fraser A.,
A. Gentles R., Goble A., Hamiln N., Harris D., Hiddled J., Hodgen G.,
A. James M., Gones L., Johnes M., Leacher S., McDonald S., McLean J.,
A. James W., Ownel S., Mungall K., Murphy L., Niblett D., Odell E.,
A. Moliver K., Ownel S., Marsen D., Quail M.A., Rabinowitech E.,
A. Rutherford W., Mungall K., Murphy L., Niblett D., Odell C.,
A. Rutherford W., Mungall K., Marken S., Stevens K.,
A. Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A. Moddward J., Volckeart G., Aerr R., Robben J., Grapmonpres B.,
A. Melleins I., Vannerreels B., Rieger W., Schaefer W., Muller-Auer S.,
A. Borzyw K., Langer I., Beck A., Lehrach H., Schaefer W., Meller-Auer S.,
A. Berr P., Zimmermann W. Wedler H., Wamburt R., Purnalle B.,
A. Maller R., Ares S., Lallare V., Mottier S.,
A. Maller R., Wanner C., Marken W., Galaure V., Mottier S.,
A. Maller R., Wanner J., Stander S., Glaure V., Mottier S.,
A. Maller R., Wanner J., Stander S., Glaure V., Mottier S.,
A. Maller R., Wanner J., Morceno S., Calladre W., Garzon A., Thode G.,
Boga R., K., Curzado L., Jimenz J., Sanher M., Pallada V.A., Garzon A., Thode G.,
A. Boga R., K., Wanner J., Shaker M., Pallada V.A., Garzon A., Thode G.,
Boga R., Carvell R., W., Waller I., Morceno S., Ammetrong J., Forsburg S.L.,
A. Shakovweki G.W., Userey D., Barrell B.G., Murse P.;
A. Shakovweki G.W., Userey D., Marsell R., Warren T., Waller S.,
A., Maller R., Maller R., Pallada V.A., Garzon A., Thode S.,
A., Shakovweki G.W., Userey D., Barrell B.G., Murse P.;
A., Shakovweki G.W., Userey D., Barrell B.G., Murse P.;
A., Waller R., Waller R., Waller R., Pallada V.A., Garzon A., Thode G.,
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ng as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Ebkaryvta; Fungi Ascomycets Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomyceteese;
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Hypothetical protein C31A2.13c in chromosome I.
SPAC31A2.13C.
                                                                                                                                                                                                                                                                                                                           (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                           91 AA.
       Pred. No. 68;
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                             0; Mismatches
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TRANSMEM 68 84 POTENTIAL.
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       100.04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 415:871-880(2002).
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                                 4; Conservative
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es 4; Conserv
Best Local Similarity
Matches 4; Conserv
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01-NOV-1995
                                                                                 1 DRAT 4
                                                                                                                                                                                                                                                                       YA4D SCHPO
009730;
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YA4D_SCHPO
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RESIDENTIALS, Serogroup A / Serocrope 4A;

MEDLINB-2022556; PubMed-1076139;

RA PERLIN J. A Montann M. James K.D., Bentley S.D., Churcher C.,

RA ALGE S.R., Worell G. L., Basham D. Chillipmyorth H.I.,

RA Algels R.M. Davies P., Devilin K., Feltwell T., Hamilan N., Holroyd S.,

RA Jagels R.M., Davies P., Devilin K., Feltwell T., Hamilan N.,

RA Malebae S., Sprate B., Moule S., Wangall R., Obatl M.A.,

RA Milchead S., Sprate B.G., Barrell B.G.,

RT Wordpate DNA sequence of a serogroup A strain of Neisseria

RE MILCHIGA 22491."

RE TOWN TOWN RASSE PERLIANS B.G., Permins J. Le can also cleave other RNA substrates such as 4.5 RNA. The Protein Component plays an substrate such as 4.5 RNA. The Protein Component Days and Strain of broadening the substrate specificity of the ribosyne (By similarity).

C. C. The Town of the S. Jaader sequence and broadening the substrate specificity of the ribosyne (By similarity).

C. C. The Town of the TNA protein RNA precurates of a cashivite cleavage of RNA, removing S.—

C. T. SERMINT: Consiste G. a cashivite CNA component (MI or rnpB) and a consistent of the SIMILARITY: BELONGS TO THE RNA PAILY.
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16-OGT-2001 (Rel. 40, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
Ribonuciease P protein component (BC 3.1.26.5) (RNaseP protein) (RNase
                                         Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria.
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Bacteria, Proteobacteria, beta subdivision, Neisseriacese, Neisseria.
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Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AA; 14288 MW; 860703F33865E0F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro IPR000100; Ribonuclease P. Bran, PR00825; Ribonuclease P. 1. ProDom, PD003629; Ribonuclease P; 1. IGREAMS; TIGR00188; Inph; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL162753; CAB83843.1; -.
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SEQUENCE 121 AA;
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                                                                                                       NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 DRAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPA NEIMB
Q9JXS6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
RNPA_NEIMB
            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EWBL outsetion the Buropean Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license egreement (See http://www.isb-sib.ch/anounce).
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050346; 1.
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last annocation update)
Ribonuclease P procein component (RC 3.1.26.5) (RNaseP protein) (RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear Mylhddrosis vitus genome."; Virology 29:181-196[1997].
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orgyia pseudotaugata multicapaid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 1; Length 104; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Punk C.J., Evans J., Harwood S.,
Robrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 1; Length 109; 100.0%; Pred. No. 81; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0: Indels
                                             HISSP; P18315; 1FWB.

TICR: MT1897;
TICR: MT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA; 12053 MW; 597E7F7137389454 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECORI-T site protein ETM homolog.
283859, CABO6138.1, -.
AE007047, AAK46168.1, -.
P18315, 1PWB.
                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%;
4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U75930; AAC59051.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 DRAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 DRAT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VETM NPVOP
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
VETM_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
RNPA NEIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of 8 bioinformatics and the Emble outstation—the European Swinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified an on-profit institutions as long as its content is in no way modified and has statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement is more removed. Usage by and for commercial or send an email to license@isb_esb_ch).
                                   CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
Xbb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Arg or Lys, and Xbb may be Pro.
CORACTOR: WANAANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEÇUENCE FROM N.A.
BELINE-27105-95-8, PubMed=9163424;
Freiberg C.A., Felley R., Bairoch A., Broughton W.J., Rosenthal A.,
Freiberg C.A., Felley B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 387:334-401(1997).
-!- SUBCELLULAR LOCATION: INLEGRAL membrane protein (Potential).
-!- SIMILARITY: STRONG, TO A.TUMEFACIENS II PLASMID TRBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid sym pNRR214a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perret \tilde{X} , "Molecular basis of symbiosis between Rhizobium and legumes.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 1; Length 125; 100.0%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 AA; 13409 MW; 42ABBD917A0AA971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
92D46CD03AA00DE4 CRC64;
                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable conjugal transfer protein trbC.
TRBC OR Y4CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00819; Peptidase M17.
Pfam; PF00883; Peptidase M17; I.
Hydrolase; Aminopeptidase; Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conjugation; Plasmid; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000068; AAB92429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y13330; CAA73771.1; -. HSSP; P00727; 1LAM. MEROPS; M17.002; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRBC RHISN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P55396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRBC RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Misinformatics and the EWBL outstainnthe European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce).
Testelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Stelenin H., Saunders N.J., Hood D.M. Forden J.F., Dodon R.M., Netchum K.A., Hood D.M. Ferenon J.F., Hodson R.M., Heit D.H. C., Owling M.A., Chies D.M., Hold R.D., Hodson R.D., Howlberg B.A., Mason H. C., Clecko, P. Parksey N.G., Pleischmann R.D., Townberg B.A., Mason M.J., Clecko, P. Parksey N.G., Blarz B.C., Citcome H., Clark B.A., Cotton M.M., Ortechas K.P., Khouri H., Qui H., Yomethewan J., Gotton M.M., Clark B.A., Mason M.M., Salaz W., Grandi G., Sun. Ganki H., Clark B.A., Salaz W., Witza M., Grandi G., Sun. C., L., Complete G. H., Mooron B.M., Rappool B. W., Venter J.C., Complete Grands on Sequence of Nelsearia meninglitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                          component plays an auxiliary but essential role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the ribozyme (By similarity) CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last aequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (BC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Rubic D. M., Ployee E., Herrero A.; strain PCC 7942 corresponds to a Rubic D. M., Ployee E., Herrero A.; strain PCC 7942 corresponds to a moba gene for univelydopterin updanine disulcated this bioaynthesis."; Submitted (MAY.1997) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: PRESUMBALY INVOINCED IN THE PROCESSING AND REGULAR TURNOVER OF INTRACLELLULAR PROCESSING. ADDRESSING AND REGULAR UNIVELULAR PROCESSING. ADDRESSING AND REGULAR TURNOVER OF INTRACLELLULAR PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extra-nucleotide from tRNA precursor. SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
                                                                                                                                                                                                                                                                                                                      --- FINCTION: RNssep catalyzes the removal of the 5'-leader sequence from pre-tWM to produce the mature 5'remmins. If can also cleave other RNA substrates such as 4'.5' RNA. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IIGRPAMs; TIGRO0188; rmpA; 1.
PROSITE; PSO00649; RIBOUCLEASE_P; FALSE NBG.
Hydroclaes; Endonuclease; ENA processing; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 1; Length 121; 100.0%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AA; 14211 MW; D4DE8C0EA865E325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein subunit (By similarity).
-!- SIMILARITY: BELONGS TO THE RNPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR000100; Ribonuclease_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00825; Ribonuclease P; 1.
Probom; PD003629; Ribonuclease P; 1.
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                                                                                                                                                                                                                                                                                               Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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SEQUENCE 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 DRAT 97
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006865;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermacophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACC clade,
Panicoideee, Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopez I., Anthony R.G., Maciver S.K., Jiang C.J., Khan S., Weeds A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
(F-ACTIN) AND BINGS TO ACTIN WONDERS.

-i SUBCELLULAR LOCATION: Cycoplasmic. As root hairs emerges and the microfilament bundles redirect to the outgrowth ADP3 concentrates at the tip of the emerging hair and remains in this position as elongation proceeds
-i-TISSUS SPECIFICITY Expressed in all tissues except pollen.
-i-SIMILARITY: BELOMOS TO THE ACTIN-BINDING PROTEINS ADP PAMILIV.
                                                                                      Gaps
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"Anan C.J., Weede A.G., Hansey P.J.;

"The maize actin-depolymerizing factor, ZmADF3, redistributes to the growing tip of elongating root hairs and can be induced to translocate into the nucleus with actin.";

Pant J. 12.1035-1044(1997).
                                                                                 ö
Query Match 100.04; Score 20; DB 1; Length 127; DB total Similarity 100.04; Pred. No. 94; Merches 4; Conservative 0; Mismatches 0; Indels Matches 4; Conservative 0; Mismatches 0; Indels
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Query Match

Query Score 20, DB 1; Length 139;

Best Local Similarity 100.04; Pred. vo. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels

Matches 4; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pollen specific expression of maize genes encoding actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE-UMY-2002 (Rel. 41, Created)
11-JUN-2002 (Rel. 41, Last sequence update)
11-JUN-2002 (Rel. 41, Last sequence update)
11-JUN-2002 (Rel. 41, Last sequence update)
ADF3 OR ABP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     depolymerizing factor-like proteins.";
Proc. Natl. Acad. Sci. U.S.A. 93:7415-7420(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                 139 AA.
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Pram; PG0041, coflln.ADF. 1.
ProDon; PD002139; Actbind cofln; 1.
SWART; SW00102; ADF. 1.d cofln; 1.
PROSITE; PS00325; ACTIN DEPCLYMERIZING; 1.
Actin-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays (Maize)
                                                                                                                                                                                                                     111 DRAT 114
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ADF3 MAIZE
ID ADF3 MAIZE
AC Q41764;
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48 DRAT 51
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Search completed: May 6, 2003, 15:01:29 Job time : 6 secs

us-09-851-422b-2.rpr

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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

(without alignments) 54.934 Million cell updates/sec May 6, 2003, 14:59:05 ; Search time 7 Seconds Run on:

US-09-851-422B-2 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 DRAT 4

Seguence:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: Pirl:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	carboxypeptidase 3	hypothetical prote	hypothetical prote		hypothetical prote	probable lipoprote	UMP kinase - Therm	vitamin D receptor	A-ORF-Q protein -	toxin gamma precur	toxin gamma precur	neurotoxin TsVII p	hypothetical prote	probable SNARE pro	hypothetical prote	probable ureB prot	hypothetical 12.2K	Salfb protein - va	hypothetical prote	hypothetical prote		hypothetical prote	iron regulatory pr	Ig heavy chain V r	hypothetical prote			probable ribonucle	ribonuclease P pro
SUMMARIES	ID	A44923	F84284	S11950	B86803	E86067	AD0919	S51096	A60912	D42525	562867	562868	S21158	B82666	559647	C83804	A70665	JQ2140	JQ1823	T10321	AC2497	AD2868	T13270	868316	E30540	H97644	T11049 '	139623	F81973	H81027
	Length DB	28 2	63 2	64 2	64 2	67 2	67 2	70 2	70 2	77 2	84 2	84 2	84 2	87 2	91 2	91 2	104 2	105 2	105 2	109 2	111 2	113 2	113 2	115 2	118 2	118 2	119 2	120 2	121 2	121 2
من	Query Match Len	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	50	20	20	20	20	20	20	20	20	20	20	50	20	20	20	50	20	50	50	20	20	20	50	20	20	20	20	50	50
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ferredoxin (import	protein kinase (EC	Ig kappa chain V-J	hypothetical prote	probable membrane	regulator of nucle	DnaK suppressor pr	probable DnaK supp	actin-depolymerizi	hypothetical prote	hypothetical hemog	hypothetical prote	hypothetical prote	dosage-dependent d	conserved hypothet	dnak suppressor pr
AH2170	T07886	540345	C83418	E87024	C82438	F81243	G82015	T02914	S72386	S07342	E72647	T01476	A64046	C82513	C84953
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ALIGNMENTS

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Cigoeiles: Rhizomore cational codes (Lustinature) (Logarica) (Logarica) (Lustinature) (Lustinature)

ö Query Match 100.0%; Score 20; DB 2; Length 28; Best Local Similarity 100.0%; Pred. No. 47; Matches 4; Conservative 0; Mismatches 0; Indels

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Gaps

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16 DRAT 19

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RESULT 2

F84284

Proportion process Wigners (Imported) - Halobacterium sp. NRC-1
Cipace: O's Peb-2001 Bequence-Evision 02-Peb-2001 #text_change 02-Peb-2001
Cipace: O's Peb-2001 Bequence-Evision 02-Peb-2001 #text_change 02-Peb-2001
Cipace: O's Peb-2001 Bequence-Evision 02-Peb-2001 #text_change 02-Peb-2001
Cipace: O's Peb-2001 Bequence-Evision 02-Peb-2001
Rigg W. V. Kennedy, S. P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, Jung, K.H.; Alam, M.; Freitas, T., The Transon, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl.
Outley, K.H.; Alam, M.; Freitas, T., Tyn-12181, 2000
A; Muchors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A; Eccence number: A81469; MUDI:20904483; PMID:1016990

A;Status: preliminary A;Accession: F84284

A;Wolecule type: DNA A;Residues: 1-63 <STO> A/Cross-references: GB:AE004437; NID:g10580814; PIDN:AAG19642.1; GSPDB:GN00138 C;Genetics: A; Gene: VNG1295H

Query Match 100.0%; Score 20; DB 2; Length 63; Best Local Similarity 100.0%; Pred. No. 1ev-0; Marches 4; Conservative 0; Mismatches 0; Indels ò

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A;Cross-references: GB:AB005174; NID:gl2518676; PIDN:AAG59001.1; GSPDB:GN00145; UWGP:ZS-AExperimental source: strain O157:H7, substrain EDL933
C;Genetico:
A;Gene: Z5325
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Grant Striber Striber Striper Str
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A:Molecule type: DNA
A:Molecule type: DNA
A:Gross-references: GB:AL513362; PIDN:CAD09374.1; PID:g16S04492; GSPDB:GN00176
C;Genetics:
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C.Species: Thermus aquaticus
C.Date: 07-Mav-1955 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
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A.Residues: 1-70 - GBLA.
A.Troces reference: BMBL:X83598; NID:g619568; PIDN:CAA58579.1; PID:g619571
A.Noces in the source is designated as Thermue thermophilus
C.Superfamily: unidine 5'-monophosphate Kinase
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A;Experimental source: strain IL1403
A;Genetics:
A;Gene: pl353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:XSS788, NID:g311223, PIDN:GAA39311.1, PID:g3980213
C;Superfamily: acyl carrier protein, acyl carrier protein homology
C;Keywords: carrier protein
F;15-64/Domain: acyl carrier protein homology (fragment) <ACP>
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Best Local Similarity
Matches 4; Conserv
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A/Molecule type: DNA
A/Regidues: 1-67 <STO>
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A; Residues: 1-64 < COI
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R;Becerril, B.; Corona, M.; Coronas, F.I.V.; Zamudio, F.; Calderon-Aranda, E.S.; Fletch acchem. J. 313, 753-766, 1996
A;Title: Toxic peptides and genes encoding toxin gamma of the Brazilian scorpions Tityu A;Reference number: S65861; MDID:96190713; PMID:961181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N'Alternate names beta-neurotoxin; neurotoxin III-11; neurotoxin III-10; toxin gamma cipecies in Tryns serulatus (Brazilan scorpton) cipecies in Tryns serulatus (Brazilan scorpton) cibate: 22-Nov-1993 sequence zevision 04-Oct-1996 #text_change 16-Jul-1999 *CACession: 821108; 339438, A39510; 332790 *R.Wattin-Eauclaire, M.F.; Ceck, B.; Ribeiro, A.M.; Diniz, C.R.; Rochat, H.; Bougis, P. FEBS Lett., 302, 220-222, 1992 *A; Ribeiro, A.M.; Diniz, C.R.; Rochat, H.; Bougis, P. A; Ribeiro, R. Mattin-Eauclaire cloning and nucleotide sequence analysis of a cDNA encoding the main A; Reference number: 52156; MULD: 9220001; PMID: 139357
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A;Cross-references: EMBL:X66256; NID:g312021; PIDN:CAA46982.1; PID:g312022
FEBS (Lett. 315, 6-8, 1993
A;Title: The genomic region encoding toxin gamma from the scorpion Tityus serrulatus con A;Reference number: 839438; MUID:94063080; PMID:8243666
A;Accession: 839438; MUID:94063080; PMID:8243666
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A;Residues: 1-84 «BEC>
A;Residues: 1-84 «BEC>
A;Residues: 1-194 «BEC>
A;Residues: 1-194 «BEC>
RNDL.866941; NID:g453105; PIDN:AMB29128.1; PID:g453106
R;Possani L.D.; Martinn B.M.; Pietcher, M.D.; Pletcher JF., P.L.
B; Biol. Chem. 266, 1991.
A;Rille: Discharge effect on pancreatic exortine secretion produced by toxins purified
A;Reference number: A39510, MULD:9113123; PMID:399589
                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin gamma precursor - Tityus bahiensis
C.Species Tityus bahiensis
C.Date: 19-Nar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C.Accession: S62868; S62861
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A;Residues; 21-81 + 2008-
R;Possani, L.D.; Martin, B.M.; Svendsen, I.; Rode, G.S.; Erickson, B.M.
Blochem. J. 209, 739-750, 1985
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                                                                                                                                                            Length 84;
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llarity 100.0%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-84 <BEC>
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A;Molecule type: mRNA
A;Residues: 1-84 <MAR>
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                                                                                                                                                                                                                             C. Species: Tityus structure.
C. Scession: S62867; S62865
C. Accession: S62867; S62865
Biochem. U. 313, 753-766; I1986
A. Title: Toxic peptides and genes encoding toxin gamma of the Brazilian scorpions Tityus A. A. Title: Toxic peptides and genes encoding toxin gamma of the Brazilian scorpions Tityus A. A. Tityus S62861; WUID: 96190713; PMID: 9611131
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F.21-821Product: toxin gamma #status predicted <4M70
F.31-81,38-57,43-62,47-64,101sulfide bonds: #status predicted
F.31-81,Modified site: amidated carboxyl end (Cys) (amide in mature form from following
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Species Gallus (aglus (chicken)
Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
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A,Note: hober Homo sapisns (man)
C;Dates: 08-Nov-1990 Hsequence_revision 09-Nov-1990 #text_change 08-Apr-1394
C;Accession: D42525
R;Johnson O6 GenBank, June 1990
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Wed_May 7 14:15:08 2003
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A;Accession: D4252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-77 <JOH>
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Matches 4; Conserv
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A, Residues: 1-84 <BEC>
A, Accession: S62865
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100.0%; Score 20; DB 2; Length 91; ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0; Indels
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Job time : 9 secs
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Best Local Similarity
Matches 4.; Conserv
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A; Introns: 39/3
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A,Gene: BH1235
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                                                                                                                     C;Genetics 15/1
C;Superfamily: scorpion neurotoxin
C;Superfamily: scorpion neurotoxin
C;Superfamily: scorpion neurotoxin
C;Superfamily: scorpion neurotoxin
F;1-20/Domain: signal sequence #stetus predicted <SIG>
F;1-20/Domain: signal sequence #stetus predicted <SIG>
F;1-20/Domain: signal sequence #stetus predicted <SIG>
F;1-18/1-20/Domain: signal sequence are sequence #stetus predicted
F;11-81,35-57,43-62,47-64/Disulfide bonds: #stetus predicted
F;81/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly
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Cibates: 18-349-2000 #text_change 20-Aug-2000
Cibates: 18-349-2000 #text_change 20-Aug-2000
Recession: 182666 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Reanonymous: The Xylella familia familions of the plant pathogen Xylella familions of the plant pathogen Xylella familions Alfacerace number Assatise for a complete list of authors see reference number Assatise for a complete list of authors see reference number Assatise.
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*Kefetence unumber: 832789; MUID:86025386; PMID:4052021
A,Accession: 832790
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C.Date: 1-128-1896 Resquence_revision 19-Apr-1996 #text_change 21-Jan-2000
C.Accession: T38617
R.Dev\land K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                         A; Molecule type: protein A; Residues: 21-81 < PO2>
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Best Local Similarity
Matches .4; Conserv
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A;Molecule type: DNA
A;Residues: 1-87 <SIM>
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A;Cross-references: EMBL:ZS0113; NID:g914878; PIDN:CAA90471.1; PID:g914891; GSPDB:GNOO0:
Afberimental source: strain 972h-; cosmid c31A2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Status: pre-liminary
A:Wolecule type: DNA
A:Residues: 1-31 «STO»
A:Residues: 1-31 «STO»
A:Roperimental source: strain C-125
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C.Species 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                A;Accession: T38611
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31, CDE2>
submitted to the EMBL Data Library, July 1995
A;Reference number: 221731
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Seguence:

Run on:

Searched:

Database

Result

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Sequence 512, Application US/10043487
Sequence 512, Application US/10043487
CENTRAL INFORMATION:
CENTRAL INFORMATION:
APPLICANT: PIERCE, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypepti
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Sequence 5 Application US/10067813

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US-0174-590-274
US-10-114-590-418
US-10-114-590-418
US-10-115-756-418
US-10-115-714-618
US-10-115-718-418
US-10-116-758-418
US-10-114-779-418
US-10-114-779-418
US-10-114-779-418
US-10-114-779-418
US-10-114-779-418
US-10-114-779-418
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        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
     DRAT 13
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Sequence 532, App
Sequence 37, Appl
Sequence 3764, A
Sequence 3663, A
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                                                                                                                                  6, 2003, 15:01:10 ; Search time B Seconds (without alignments 43.143 Willion cell updates/sec
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                        GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen_Ltd.
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US-09-664-761-3163

US-10-102-806-807

US-09-864-761-34962

US-09-864-761-34962

US-09-864-761-34962

US-09-64-864-761

US-09-989-298-274

US-09-999-298-274

US-09-999-298-274

US-09-999-275-274
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US-09-993-687-274
US-09-989-734-274
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Maximum Match 100*
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 58153, Application US/09864761
Patent No. US2002004876331
GRHEAL INFORMATION: Parm. Sharron G.
APPLICANT: Parm. Carlot G.
APPLICANT: Harbard G.
APPLICANT: Harbard G.
APPLICANT: Harbard G.
APPLICANT: Harbard G.
APPLICANT: Chen. Wendberg G.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL POR
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INCORMATION: EXPRESSED IN FEATA, SIGNAL = 1.9
INCORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
INCORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
INCORMATION: EXPRESSED IN LING SIGNAL = 1.7
INCORMATION: EXPRESSED IN BANK MARKAL = 1.7
INCORMATION: EXPRESSED IN HARKER SIGNAL = 1.7
INCORMATION: EXPRESSED IN HARKER SIGNAL = 2.6
INCORMATION: EXPRESSED IN HEARER SIGNAL = 2.6
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION UNDER: 036 60/236,359
PRIOR APPLICATION UNDER: 036 60/236,359
PRIOR APPLICATION UNDER: 057/081/00666
PRIOR APPLICATION UNDER: PCT/081/00667
PRIOR APLIANG DATE: 2001-01/081/00667
PRIOR APLIANG DATE: 2001-01/081/00667
PRIOR APLIANG DATE: 2001-01/081/00669
PRIOR APLIANG DATE: 2001-01/081/00669
PRIOR APLIANG DATE: 2001-01/081/00668
PRIOR APLIANG DATE: 2001-01/081/00668
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PRIOR APLIANG DATE: 2001-01/081/00668
PRIOR APLIANG DATE: 2001-01/081/00661
PRIOR APLIANG DATE: 2001-01/081/00670
PRIOR PLIANG DATE: 2001-01/081/00670
PLIANG SADING S
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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US-09-864-761-37634
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TITLE OF INVALORISES AND THEIR USES
TITLE REPRESENCE 6277 CYTOCHONE 7450 OXYGENASES AND THEIR USES
CHRRMT APPLICATION UNDERR. US/10/142,231
CURRENT APPLICATION UNDERR. US/165,250
PRIOR APPLICATION UNDERR. 1999-11-12
NUMBER OF SEQ ID NOS: 95
SOUTHWER PARENTER 1999-11-12
SOUTHWER PARENTER 1999-11-12
LENGTH S. DARRIER 1999-11-12
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       TITLE OF INVENTION: mammalian polypeptides
FILE BREREMENE BA798
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT PILLNE DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
PRIOR APPLICATION NUMBER: US 60/261,130
NUMBER OF SEO.ID NOS: 561
SOTTWARE: Patentin vergion 3.1
SEQ ID NO 532
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Patent No. US20020048763A1
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Publication No. US20030077796A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-532
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Best Local Similarity 100.
Matches 4; Conservative
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; ORGANISM: Taxus cuspidata
US-10-142-231-37
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/NET: SITE LOCATION: (18)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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             TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                       PILE REPRESENTE PRICES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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LOCATION: (67)
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F: P15293, EVALUE 5.00e-01
F: BF364203.1, EVALUE 9.00e-20
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IN EXPRESSED IN NOTIT LIVER, SIGNAL = 7.1
IN EXPRESSED IN NOTIC, SIGNAL = 5.2
IN EXPRESSED IN LIVE, SIGNAL = 6.4
IN EXPRESSED IN LIVE, SIGNAL = 4.4
IN EXPRESSED IN PARKOW, SIGNAL = 5.7
IN EXPRESSED IN HEART, SIGNAL = 5
IN EXPRESSED IN HEART, SIGNAL = 5
IN EXPRESSED IN HEART, SIGNAL = 5.7
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                                                                        RELOR ALLIA MAINE DATE: JOUGO 12-03 PRIOR FLITAMING DATE: JOUGO 12-04 PRIOR FLITAMING DATE: JOUGO 12-05 PRIOR FLITAMING DATE: JOUGO 12-05 PRIOR FLITAMING DATE: JOUGO 12-05 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR PLING DATE: JOUGO 10-04 PRIOR FLITAMING DATE: JOUGO 10-04 PRIOR FLITAMIN
APPLICATION NUMBER: US 60/180,312
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SOFTWARE: Annomax Sequence I
SEQ ID NO 36163
LENGTH: 66
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ORGANISM: Homo sapiens
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Matches 4; Conserv
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APPLICANT: Chen, Wensheng TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REPERENCE: Aecamica-X-1

Sequence 34962, Application US/09864761 Patent No. US20020048763A1

Gaps ô

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.

CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312

Sequence 807, Application US/10102806 Publication No. US2003054421A1 GENERAL INFORMATION: APPLICANT: Rosen et al.

US-10-102-806-807

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Ouery Match

100.0%; Score 20; DB 10; Length 72;

Bert Local Similarity 100.0%; Pred. No. 1.5e+06.

Matches 4; Conservative 0; Mismatches 0; Indels
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SED ID NO 34962
LENGTH: 72
                                  PRIOR PLING DATE: 2006.05-26 "CATALOGUE PRIOR PRIOR PLING DATE: 2006.06-09 - 20 "CATALOGUE PRIOR APPLICATION NUMBER: US 90/612/36 PRIOR APPLICATION NUMBER: US 60/236/35 PRIOR PLING DATE: 2006.10-09 - 27 "CATALOGUE PRIOR PLING DATE: 2006.10-09 - 27 "CATALOGUE PRIOR PLING DATE: 2006.10-09 - 27 "CATALOGUE PRIOR PLING DATE: 2006.10-130 PRIOR PLING DATE: 2001.01-30 PRIOR PRIOR PLING DATE: 2001.01-30 PRIOR PRI
US 60/207,456
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PRIOR FILING DATE: 2001-01-29
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INFORMATION: EST HUMBAN HIT: AM997711.1, EVALUE 7.00e-28
INFORMATION: SWISSPROT HIT: POBS47, EVALUE 2.00e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 78;
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IN LUNG, SIGNAL = 3
IN BRAIN, SIGNAL = 1.9
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SEQ 1D NO 34713
LENGTH: 78
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100.0%; Pred. No. 1.7e+02;
iive · 0; Mismatches 0;
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BXPRESSED IN HBLA, SIGNAL = 8.
EXPRESSED IN PLACENTA, SIGNAL EXPRESSED IN HEART, SIGNAL = 1.
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ORGANISM: Homo sapiens
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Matches 4, Conserv
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OTHER INFORMATION:
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Sequence 34713, Application US/09864761 Patent No. US20020048763A1

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GENERAL INFORMATION APPLICANT: Penn, S

APPLICANT:

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APPLICANT: William: I. Transper Control of the Management of the M
Sequence 274, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paoni, Nicholas F.
Sewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
                                                                                                                                                                                                                                          Ferrara, Napoleone
Fong, Sherman
                                                                                                                                                                                                                                                                                                                                      Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                         Gerber, Hanspeter
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Napier, Mary A.
                                                                                            APPLICANT: Ashkenazi, Avi J
                                                                                                                     Baker, Kevin P.
Botstein, David
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                                                                                                                                                                                   Desnoyers, Luc
Eaton, Dan L.
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LOCATION: (misc_feature
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION (191)
OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids
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LOCATION: (813)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LCCATION: (37)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: Resen et al.
TITLE OF INVENTION: Nucleic Acids, Proceins, and Antibodies
FILE REPERENCE: PCODE.
CURRENT APPLICATION NUMBER: US/09/764,847
FILE ADDICATION AND EXPENSED TO THE APPLICATION NUMBER: 2001-01-17
FILE ADDICATION data removed - consult PAIM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTMARS: Parentin Ver. 2.0
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                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERDECE: PC009C1.
CURRENT PAPLICATION NUMBER: US/10/092,154
CURRENT PILLIG DATE: 2002-03-07
NUMBER OF SEO ID NOS: 2003-07
NUMBER OF SEO ID NOS: 2003-05
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 620, Application US/09764847
Patent No. US20020132767A1
                                                                                   ; Sequence 620, Application US/10092154; Publication No. US20030054375A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-09-992-598-274
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US-09-764-847-620
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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PPLICATION NUMBER: 60/088734
ILING DATE: 1998-06-10
PPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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FTLING DATE: 1998-06-10
APPLICATION NUMBER: 60/08826
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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LING DATE: 1998-06-12
LICATION NUMBER: 60/089440
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
JICATION NUMBER: 60/088326
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LICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089514
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ING DATE: 1998-06-17
LICATION NUMBER: 60/089538
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APPLICATION WIMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089947
                       LICATION NUMBER: 60/088167
                                FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/08861
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ICATION NUMBER: 60/089598
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FILING DATE: 1998-06-24
APPLICATION WHBER: 60/090435
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
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APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
                           ILING DATE: 1998-06-05
PPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/08810
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APPLICATION NUMBER: 60/08824
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APPLICATION NUMBER: 60/08826
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TLING DATE: 1998-06-11
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090254
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PRIDORICE6
CURRENT APPLICATION NUMBER: US/09/989, 293A
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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LING DATE: 1998-05-28
PALICATION NUMBER: 60/087607
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
                                                                                                                                                                                                                              Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                   Noy, Margaret Ann
Stewart, Timothy A
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                                                                                                                          Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                    aoni, Nicholas F
                                                                                               Gerber, Hanspeter
                                                                                                                                                                                                                                                                                         Cliavin, Ivar J
                                                                                                                                                                                                                                                                                                                                                                                                                            Stewart, ...
Stewart, ...
Daniel
                                                                                                                                                                                                                                                         Surney, Austin
                                                                                                                                                                                                                                                                                                                             pier, Mary A.
                                                                                                                                                                                          Godowski, Paul
                                                               ong, Sherman
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| APPLICANT: Numas, Daniel | APPLICANT: Numas, Numas, Cont. | APPLICANT: Numas, Numas, Daniel | APPLICANT: Numas, Numas, Daniel | APPLICANT: Numas, Daniel | APPLICANTON | APPLICA
    Grimaldi, J. Christopher
                                                                                                                                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                          Paoni, Nicholas F.
                                                                                              Napier, Mary A.
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100.0%; Score 20; DB 9; 1
Best Local Similarity 100.0%; Pred, No. 1.8e-02;
Macches 4; Conservative 0; Mismatches 0;
                                                                             PRIOR PLILING NUMBER: 60/040472

REIGR FILLING DINER: 1,996-66-24

REIGR FILLING DINER: 1,996-66-24

REIGR PELLING DINER: 1,996-66-25

REIGR PELLING DINER: 1,996-66-26

REIGR PELLING DINER: 1,996-67-20

PRIOR APPLICATION NUMBER: 60/09154

PRIOR PELLING DINER: 1,996-67-20

PRIOR APPLICATION NUMBER: 60/09154

PRIOR APPLICATION NUMBER: 60/09154

PRIOR PELLING DINER: 1,996-67-67

PRIOR APPLICATION NUMBER: 60/09154

PRIOR PELLING DINER: 1,996-67-67

PRIOR APPLICATION NUMBER: 60/09154

PRIOR PELLING DINER: 1,996-67-67

PRIOR PELLING DINER: 1,996-67-67

PRIOR PELLING DINER: 1,996-67-67

PRIOR PELLING DINER: 1,996-07-67

PRIOR APPLICATION NUMBER: 60/091982

PRIOR PELLING DINER: 1,996-07-67

PRIOR APPLICATION NUMBER: 60/091982
                         PLICATION NUMBER: 60/090445
LING DATE: 1998-06-24
PLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
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Sequence 274, Application US/09989735
Publication No. US2020193299A1
APPLICATION NO. MEMBERAZI, AV. J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.

-09-989-735-274

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Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey errara, Napoleone Desnoyers, Luc

Eaton, Dan L.

APPLICANT: APPLICANT:

Godowski, Paul

APPLICANT: APPLICANT: APPLICANT:

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FILTING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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LICATION NUMBER: 60/090431
ING DATE: 1998-06-24
                                                                             FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
                                                                                                                                         APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088826
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
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LICATION NUMBER: 60/090429
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ILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
                                                           APPLICATION NUMBER: 60/088742
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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PPLICATION NUMBER: 60/089514
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LING DATE: 1998-06-17
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LING DATE: 1998-06-17
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PLICATION NUMBER: 60/089908
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LING DATE: 1998-06-19
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                    60/088738
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                                      LING DATE: 1998-06-10
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PRIOR PAPLICATION NUMBER: 60/090540
PRIOR PLING DATE: 1998-06-34
PRIOR PLING DATE: 1998-06-34
PRIOR PLING DATE: 1998-06-34
PRIOR PLING DATE: 1998-06-34
PRIOR PLING DATE: 1998-06-36
PRIOR PLING DATE: 1998-06-36
PRIOR PLING DATE: 1998-06-35
PRIOR APPLICATION NUMBER: 60/090659
PRIOR PLING DATE: 1998-06-35
PRIOR PLING DATE: 1998-06-35
PRIOR APPLICATION NUMBER: 60/090659
PRIOR PLING DATE: 1998-06-35
PRIOR RELING DATE: 1998-06-36
PRIOR RELING DATE: 1998-07-01
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-03
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Query Match 100.0%; Score 20; DB 9; Length 86; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels

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SSULT 14

Paoni, Nicholas F. Roy, Margaret Ann

APPLICANT: APPLICANT:

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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088876
FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
                                                     ON NUMBER: 60/088826
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FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090431
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TILING DATE: 1998-06-24
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PLICATION NUMBER: 60/090557
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                                                                              1998-06-10
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                                                                                                       REALOR REPLICE REPLICE
                                                                                                                     APPLICANT: Zhong, Zemin mining Trille OP INTERNATION Secreted and Transmembrane Polypeptides and Nucleic Trille OP INTERNATION: Secreted and Transmembrane Polypeptides and Nucleic Trille OP INTERNATION: Action Encoding the Same FRIENCENTON: Action Encoding the Same CURRENT PRINGE TRIPS (2014) 1-14
CURRENT APPLICATION NUMBER: US/09/990.444
PRING REPLICATION NUMBER: 60/04997
PRING RELING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1597-10-17

R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R PEDICACTION NUMBER: 60/06511

R FILING DATE: 1997-11-13

R PILING DATE: 1997-11-13

R PILING DATE: 1997-11-13
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PLICATION NUMBER: 60/088026
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PPLICATION NUMBER: 60/088212
ILING DATE: 1998-06-05
PPLICATION NUMBER: 60/088217
ILING DATE: 1998-06-05
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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LING DATE: 1998-06-04
PLICATION NUMBER: 60/088029
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PLICATION NUMBER: 60/088030
LING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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LING DATE: 1998-02-25
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PLICATION NUMBER: 60/087106
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PLICATION NUMBER: 60/088326
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PLICATION NUMBER: 60/088167
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PLICATION NUMBER: 60/088202
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LICATION NUMBER: 60/088655
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                            Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Stewart, Timothy A. Tumas, Daniel
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APPLICATION NUMBER
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Acids Encoding the Same
                                                                                                                    BRIGH APPLICATION NUMBER (6.10, 612, 6.10)

BRIGH APPLICATION NUMBER (6.10, 625, 6.10)

BRIGH APPLICATION NUMBER (6.10, 667, 10)

BRIGH APPLICATION NUMBER (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                          FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/091478
FILTING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILLING DATE: 1998-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
                            80/090678
                                                                                             APPLICATION NUMBER: 60/090690
                                                                                                                              FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/090863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US20020197674A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          errara, Napoleone
1998-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1998-07-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kljavin, Ivar J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danie]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-989-730-274
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PRIOR FLICK DATE: 1999-66-19
PRIOR FLICK DATE: 1999-66-19
PRIOR FLICK DATE: 1999-66-10
PRIOR PRIOR FLICK DATE: 1999-66-10
PRIOR FLICK DATE: 1999-66-10
PRIOR PRIOR PRICKATION WINNERS: 60/09046
PRIOR PRICKATION WINNERS: 60/09046
PRIOR PRICKATION WINNERS: 60/09046
PRIOR PRICKATION WINNERS: 60/09049
PRIOR PRICKATION WINNERS: 60/09049
PRIOR PRICKATION WINNERS: 60/09044
PRIOR FLICK DATE: 1999-66-19
PRIOR PRICKATION WINNERS: 60/09044
PRIOR FLICK DATE: 1999-66-19
PRIOR PRICKATION WINNERS: 60/09044
PRIOR PRICKATION WINNERS: 60/09064
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PRIOR APPLICATION NUMBER: 6//090695
PRIOR FILING DARE: 1989-06-25
PRIOR FILING DARE: 1989-06-25
PRIOR FILING DARE: 1989-06-25
PRIOR PILING DARE: 1989-06-26
PRIOR PLING DARE: 1989-06-20
PRIOR PLING DARE: 1989-07-07

Ouery Match 100.04, Score 20; DB 9, Length 86; Deet Local Similarity 100.04; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; G

Search completed: May 6, 2003, 15:04:53 Job time : 9.3333 BecB

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 6, 2003, 14:59:30 ; Search time 6.4 Seconds (Without alignment) 16:389 Million cell updates/sec Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-851-422B-2 20 1 DRAT 4 Title: Perfect score: Sequence: Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued perents A.A. CONB. pep.*

21. /CGDZ 6/ptcdate/l/iaa/SA. CONB. pep.*

22. /CGDZ 6/ptcdate/l/iaa/SA. CONB. pep.*

31. /CGDZ 6/ptcdate/l/iaa/SA. CONB. pep.*

41. /CGDZ 6/ptcdate/l/iaa/SA. CONB. pep.*

51. /CGDZ 6/ptcdate/l/iaa/SA. pep.*

51. /CGDZ 6/ptcdate/l/iaa/SA. Davkfileal.pep.*

61. /CGDZ 6/ptcdate/l/iaa/SA. Davkfileal.pep.*

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	ilda	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	\pp]i	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App	App	App	App	Appl
c	18,	3,	16,	13,	83	11,	12	.09	9	9	60	9		15,	10,	21,	51,	51,	93,	93,	93,	93,	114	114	114	114,	98,
Description	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence				Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	
. di	US-08-222-851-18	US-08-797-842-3	US-08-952-127-16	US-08-952-127-13	US-08-817-811-83	US-08-797-842-11	US-08-797-842-12	US-07-956-700B-60	US-08-476-537-60	US-08-485-607-60	US-08-475-879-60	US-09-433-043B-60	US-07-737-736B-3	US-09-187-789-15	US-09-139-600-10	US-08-480-473B-51	US-08-915-213-51	US-09-235-217-51	US-08-276-852-93	US-08-899-575-93	US-08-899-575-93	PCT-US95-08743-93	US-08-276-852-114	US-08-899-575-114	US-08-899-575-114	PCT-US95-08743-114	US-08-276-852-98
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Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	20	50	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	50	20	50	20	50	20	50	50	50	20
Result No.	п	7	e	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27

Seguence 98, Appl	Sequence 98, Appl	Seguence 98, Appl	Seguence 5, Appli	Sequence 6, Appli	22,	Sequence 4, Appli	Sequence 28, Appl	Sequence 3, Appli	49,	Sequence 7, Appli	7,	Sequence 7, Appli	7,	12,	Sequence 36, Appl	Patent No. 5223425	Sequence 4, Appli
US-08-899-575-98	US-08-899-575-98	PCT-US95-08743-98	US-09-419-459-5	US-09-419-459-6	US-09-187-859-22	US-08-959-382-4	US-09-215-221-28	US-08-994-962-3	US-08-576-626A-49	US-07-991-867B-7	US-08-107-755A-7	US-08-544-332-7	US-09-370-861A-7	US-09-384-162-12	US-08-861-774E-36	5223425-6	US-08-658-277-4
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108	108	108	109	109	110	125	132	133	155	163	163	163	163	184	215	222	226
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ALIGNMENTS

RESULT 1	
US-08-222-851-18 Sequence 18, Application US/08222851 : Parent No. 5723128	2851
GENERAL INFORMATION:	
; APPLICANT: CLAYBERGER, CAROL A.	. А.
; APPLICANT: KRENSKY, ALAN M.	
-	
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOC	CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
	ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43	
CORRESPONDENCE ADDRESS:	
, ADDRESSEE: MORRISON & FOERSTER	STER
STREET: 2000 PENNSYLVANIA AVENUE, NW. STE 5500	AVENUE, NW, STE 5500
CITY: WASHINGTON	
; STATE: DC	
COUNTRY: USA	
; ZIP: 20006-1812	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	9
; OPERATING SYSTEM: PC-DOS/MS-DOS	IS-DOS
; SOFTWARE: Patentin Release #1.0, Version #	#1.0, Version #1.30
CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/08/222,851	222,851
PILING DATE: 05-APR-1994	
CLASSIFICATION: 424	

CALGASTFICATION: 444.
ATTORNEY/AGRAT INFORMATION: ANAE: MILLAMA, ROBERT A. REGISTRATION NUMBER: 36.217
REFERENCE/DOCKET NUMBER: 28600-20200.22
TELEPHONE: (202) 494-0792
TELEFRX: (202) 494-0792
TELEFRX: (202) 494-0792
TELER: 90-4030 MERRIPORERSHSH
INPORMATION POS SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids

Query Match 100.0%; Score 20; DB 1, Length 4; Best Local Smilarity 100.0%; Pred. No. 1.99-46; Matches 4; Conservative 0; Mismatches 0; Indels Matches 4; Conservative 0; Mismatches 0; Indels single TYPE: amino acid STRANDEDNESS: sinc TOPOLOGY: linear US-08-222-851-18

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Gaps ö

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6211336thwestern Hwy., Suite 410
ZIP: 48334
COMPUTER READABLE FORM:
WEDING TYPE: Floppy disk
COMPUTER: IN PP C comparatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DIAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48334
COMPUTER RABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPATIO SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/952,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08952127
Patent No. 6211318
GENERAL IMPONATION:
APPLICANT: SILIOL, Yosef
APPLICANT: Callin, Panilo A.
APPLICANT: Collins, Prancis S.
ITILE OF INVENTION: APPLIANCIECTASIA GENE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 31; Matches 4; Conservative 0; Mismatches
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FILING DATE
CLASSIFICATION: 530
ATTORNEY/ABENTINEDATION:
NAME: KODI, Kenneth I.
REGISTRACION NUMBER: 30, 995
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                   CLASSIFICATION: 530
ATCORRY/CAGRIT INFORMATION:
NAME: KGID, KERNER: 30,995
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION: LNFDRAMITON:
TELEBHONE: 810-539-5055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 810-539-5055
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-952-127-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DRAT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                   Sequence 3, Application US/08797842
Sequence 3, Application US/08797842
Parent No. 5923706

TITLE OF INVENTION: Anibodies specific for a haemostatic protein,
TITLE OF INVENTION: their use for isolating intact protein, heemostatic compositic
TITLE OF INVENTION: of proteolytic cleavage products of the protein
CORRESPONDENCE. ADDRESS:
ADDRESSEE: Wicheelson and Wallace
STREET: Parkway 109 Office Center, 328 Newman Springs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 18M PC
COMPUTER: 18M PC
CORRACTING STSTEM: MS-DOS, Mindows 6
CURRANT REPLICATION DATA:
FULLING DATE: 10-Feb-1997
CLASSIFICATION NAMER: US/08/797,842
FLING DATE: 10-Feb-1997
FLING DATE: PEPLICATION DATA:
FULLING DATE: PEPLICATION DATA:
MANNE: MICHARATON: 8199
ATTORNEY/AGENT INFORMATION:
NAME: MICHARATON: PECET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 20; DB 2; Length 16; Bet Local Similarity 100.0%; Pred. No. 26; Marches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM_TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6211336thwestern Hwy., Suite 410
STRTE: Farmington Hills
STRTE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08952127
PREER NO. 621136
GENERAL INFORMATION:
PAPLICANT: SHILOH, Yose
APPLICANT: Tagle, Danilo A.
PAPLICANT: Colline, Francis S.
ITILE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOhn K. Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: Stitching-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (908)530-6671
TELEPAT. (908)530-5694
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                    CITY: Red Bank
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 DRAT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-952-127-16
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-797-842-3
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Koenraad et al Antibodies appecific for a haemostatic protein, haltbodies appecific for a haemostatic compositiv their use for isolating intact protein, haemostatic compositiv of proteolytic cleavage products of the protein
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                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM MS-DOS, Windows for Workgroups 3.11
SOFTWARE MICROSOFF Word for Windows 6
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/797,842
FILING DATE: 10-Feb-1997
CLASSIFFCATION: 530
FRIOR APPLICATION DATA.
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/381,891
FILING DATE: Feburary 9, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELOW, Peer L.
RAGISTRATION WUMBER: 30090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 2; Length 40; Ilarity 100.0%; Pred. No. 65; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDTUM TYPE: 3 1/2°1.44 MByte IBM compatible diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDULW TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
COMPUTER: IBM PC
                                                                                                                                         ADDRESSEE: Michaelson and Wallace STREET: Parkway 109 Office Center, 328 Newman Springs STREET: Road, P. O. Box 6489 CITY: Red Bank STREET: OFFICE STREET: OFFICE STREET: OFFICE STREET: OFFICE STREET: OFFICE STREET: OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Farkway 109 Office Center, 328 Newman Springs STREET: Red Bank P. 0. Box 8489 CITY: Red Bank STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michaelson and Wallace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mertens, Koenraad et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/08797842; Patent No. 5932706; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)530-6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (908) 530-6584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 4 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (908)530-6584
INFORMATION FOR SEQ ID NO:
                                      TITLE OF INVENTION: ALC:
TITLE OF INVENTION: The
TITLE OF INVENTION: OF
INVESTION OF
CORRESPONDENCE 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAELSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Ant.
TITLE OF INVENTION: the
TITLE OF INVENTION: of
INVENTION: of
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: MICHAELEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 4; Conserv
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , HYPOTHETICAL:
US-08-797-842-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                 07701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 DRAT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-797-842-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                            Omery Match 100.0%; Score 20; DB 4; Length 21; Beet Local Similarity 100.0%; Pred. No. 34; Matches 4; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP...7710
COMPUTER READABLE FORM:
WEDLIN TYEE: Bloppy disk
WEDLIN TYEE: BLOPPY COMPACTION
COMPUTER: IMP FO. COMPACTION
OPERATING SYSTEM: CO-TOOK/MS-DOS
SOFTWARE: Retenil Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
FLING DATE: 14-APR-1997
CLASSIFCATION: 14-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHETIC PEPTIDES AND VACCINES COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37,642
37,642
FBRC:005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/08797842
; Patent No. 5932706
                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/08817811
Patent No. 6174528
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT COOPET, Juan A.
APPLICANT RELE WENDY A.
APPLICANT GOOD, MICHAEL F.
APPLICANT GOOD, MICHAEL F.
TITLE OF INVENTION COMPRISING
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ANDRESS:
ADDRESSES: ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REPERENCE/DOCKET WUMBER: FBI TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Houston
STATE: Texas
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-797-842-11 ·
                                                                                                                                                                                                                                                  7 DRAT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-817-811-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRAT 4
                                                               US-08-952-127-13
                                                                                                                                                                                                        1 DRAT 4
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100.0%; Score 20; DB 1; Length 44; 100.0%; Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                     Applicative mober: Haselkorn and Plotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
TITLE OF INVENTION: Cathorylase
NUMBER OF SECRETORS: 116
CORRESPONDENCE ADDRESS: 116
ADDRESSER: ARMOLG WIRE & DIRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 60, Application US/08485607
; Patent No. 5795627
; PAREAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING UALE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 10,21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E No. 5756290thrup
REGISTRATION UMBER: 3756290thrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALDLAS FORM:
HEDITH TYPE: Ploppy bisk
COMPUTER: 13M PC COMPUTED:
OFFRATING STREM: PC-DOS/MS-DOS
SOFTWARE: AGCII-DOS
CURRENT APPLICATION DATA
APPLICATION WOMBER: US/08/476,537
                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/08476537
Patent No. 5756290
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: AF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 amino acida
                                                                                                                           Conservative
            ; MOLECULE TYPE: Peptide
US-07-956-700B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-476-537-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRAGO 321
STREET: 321
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino acid
STRANDEDNESS: Si
                                                                                                  Local Similarity
hes 4; Conserv
                                                                                                                                                                                                                 25 DRAT 28
                                                                                                                                                                      1 DRAT 4
                                                                                                                                                                                                                                                                                                           US-08-476-537-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRAT 4
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US-08-485-607-60
                                                                                Query Match
                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CORRATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
SOFTWARS: MICROSOFF Ward for Windows 6
CURRENT APPLICATION DATA:
APPLICATION NOWER: US/08/797,842
FILING DATE: 10-Peb-1997
FLING DATE: 10-Peb-1997
FLING APPLICATION EATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NOWER: 08/381,831
FILING DATE: FEBURARY 8, 1995
ATTORNEY, AGRETING MARKER: SCIENCING-S
REGISTRATION WINDER: SCIENCING-S
TELEPHONEX-CANDON NURSHARION:
TELEPHONEX: (908)530-6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 20; DB 2; Length 40; Best Local Smilarity 100.0%; Pred. No. 65; Manaches 4; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60, Application US/07956700B
Parent No. 5539021
Parent No. 5539021
APPLICAWT: ROBORT HABELKOIN and PAOLT Gornicki
APPLICAWT: ROBORT HABELKOIN and PAOLT GORNICKI
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-Coh
WINGER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Arnold, White & Durkee
TYREET: 321 No. 5539032th Clark Street
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPENATURE STREAMS.
COPENATURE STREAMS.
CURRENT APPLICATION DATA.
APPLICATION NUMBER. US/07/956,700B
FILING DATE. 1992100.2
CLASSIPCATION: 800
ATOMNEY AGENT INPORATION.
NAME: Thomas E No. 529902hrup
REGISTRATION NUMBER: 33,268
REPERANTON NUMBER: 31,268
TELECOMUNICATION INPORMATION:
TELEPANE: 1-12.744-4090
TELERAX. 1-112-775-4499
INPORMATION POR SEG ID NO: 60:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: ASCII-DOS
                                                                                                                                                                                                                                                                                                                                          TELEFAX: (908)510-6584
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                          (908) 530-6671
(908) 530-6584
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60610
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us-09-851-422b-2.rai

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Sequence 60, Application US/09433043B

PRESENT NO 619391CALL INCOMPATION

GENERAL INCOMPATION:

APPLICANT HASHLKORN, ROBERT

APPLICANT HASHLKORN, ROBERT

TILLS OF INVERTION: CHANDRANGE TRAIL AND PLANT ACETYL-COA CARBOXYLASE

TILLS OF INVERTION: CHANDRANGE 100,09/43,043B

CURRENT APPLICATION NUMBER: 00/475,079

PRICE FILING DATE: 1999-10-25

FRICE FILING DATE: 1999-10-02

NUMBER: 05 SOFTHANE: PREDICTION NUMBER: 07/996,700

PRICE FILING DATE: 1999-10-02

SOFTHANE: PREDICTION NUMBER: 07/996,700

FRICE FILING DATE: 1999-10-02

SOFTHANE: PREDICTION NUMBER: 07/996,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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O'THEN INFORMATION: Description of Artificial Sequence: Synthetic
O'THEN TROCAMATION: Peptide
US-09-433-0438-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3. Application US/07737736B
Patent No. 5260199
GENERAL INFORMATION:
APPLICANT: Beliaca, Hector F.
APPLICANT: Rose, Tray K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
NUMBER OF SEQUENCES. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 20; DB 2; Length 44; Bet Local Similarity 100.0%; Pred. No. 72; Marches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE: 10/21/92
ATTOWNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
                                                                                                                REFRENCE/DOCKET NUMBER: ARCD 1058
TELECHONINITORION INFORMATION:
TELEBRANE: 1-312-744-0099
INTELERK: 1-312-755-4489
INTEREX: SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          44 amino acids
                                                                                                                                                                                                                                                                                                            TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-475-879-60
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US-09-433-043B-60
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US-07-737-736B-3
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APPLICANT: Robert Haselkorn and Plotr Gornicki
APPLICANT: Robert Haselkorn and Plotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
ITLE OF INVENTION: Carboxylase
NUMBER DF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 211 No. 5972644 5786170th Clark Street
CITTY: Chicago
STRATE: 111inois
COMPUTES READABLE FORM:
MEDIUM TYPE: READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTES READABLE FORM:
MEDIUM TYPE: GOSSIMS: NO. 5077644 57899
SOFTHARE ACTICATION NUMBER: US/08/475,879
FILING DATE: 07-UN-1995
PRICASIPTATION NUMBER: US/08/475,879
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NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSER: ATAOLd, White & Durkee
STREET: 31 No. 5/92627th Clark Street
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCIL DOS
CORRENT APPLICATION DATA:
CHRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/485,607
FILING DATE: US/08/485,700
ATTORNEY/AGENT INFORMATION:
REFERENCE/COCCUT NUMBER: ARCD: 058
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SECULOMO: 60:
                                                                                                                                                                                            ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COmparible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5972644
Patent No. 5972644 5786170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) TOPOLOGY: Linear
) MOLECULE TYPE: Peptide
US-08-485-607-60
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CORRESPONDENCE ADDRESS

us-09-851-422b-2.rai

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US-09-139-600-10

US-09-139-600-10

Sequence 10 Application US/09139600

Percent No. 46:3728

GENERAL HROWANDER PRAINT SERVEN

REPLICANT: FERRANGE-Albent, Teresa

REPLICANT: FERRANGE-Albent, Teresa

TITLE OF INVENTION: AND METHOD OF USE

TITLE OF INVENTION: AND METHOD OF USE

FILE REPRENCE: 480140,434

CURRENT PILLING DATE: 198-09-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 10

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                                                                                                                                                                                                                                                100.0%; Score 20; DB 4; Length 89; 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 6, 2003, 15:04:06 Job time: 7.4 secs
                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 4; Conservative
                                                                                                ; ORGANISM: Mus musculus
US-09-187-789-15
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STREET, 411 EAST R. Schwartz, Esq., c/o Quarles & Brady STREET, 411 EAST Wisconsin Avenue CITY. Milwaukee STATE: Wisconsin COUNTRY: U.S.A. ZIP: S10-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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PUBLICATION INFORMATION;
ATTHORS: MADOINEL! Donald P.
AUTHORS: Mangeledorf. Donald P.
AUTHORS: Mangeledorf. David J.
AUTHORS: Hauseler: Mark R.
AUTHORS: Hauseler: Mark R.
AUTHORS: Organish Receptor Complementary DNA
TITLE: Molecular Cloning of Complementary DNA
TITLE: Chence
OUGHRAL: Science
OUGHRAL: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.us,
-hon 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
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DATE: March 6-1987
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Sequence 15. Application US/09187789

Beginnen 2. Application US/09187789

Bench No. 2340740

Bench No. 2340740

Bench No. 2340740

APPLICANT Alment. Ends S. Alment. Teresa

APPLICANT Fernands Alment. Teresa

TITLE OF INVENTION: ADASMSE-14, AN ARQUITC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHORS OF USE

CURRENT APPLICANT WOMER. US/09/187, 789

NUMBER OF SEQ. ID NOS: 78

1 DRAT 4

ò 셤 RESULT 14 US-09-187-789-15

SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 15 LENGTH: 89

Human immune/haema Human gheromone re Human D2H binding Non-A non-B hepati Arabidopsis thalia

Human vitamin D re Human 5' EST relat Arabidopsis thalia

colon

Propionibacterium Taxus cuspidata RT Propionibacterium Propionibacterium

Propionibacterium

Propionibacterium Propionibacterium Propionibacterium Propionibacterium Pepiide #443 enco Human nervous syst Protein #4335 enco Human bazin expres

Peptide #4424 enco Peptide #4533 enco Peptide #4309 enco Human peptide enco Human overian anti Human colon cancer Human ORPX ORF688

Human secreted pro Human peptidase-li Propionibacterium

OM protein -

Run on:

Seguence:

Searched:

Database

Result ģ

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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; NHC; immunosupressant; graft versus host disorder; transplantation; therapy; class I MHC.
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AAC93158
AAY93158
AAC56794
AAG56794
AAM87857
AAB32462
ABB11187
AAW74045
AAG07755
AAG47989
                                                                                                                                                                                               AMUG2815
AMUG2806
AMUG2806
AMUG380
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  $\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\tince}\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\texi}\text{\text{\text{\text{\text{\texi}\text{\text{\texi}\text{\text{\text{\texit{\texi}\text{\text{\texit{\texi}\tint{\texit{\texit{\texi}\tint{\texitint{\texit{\texi}\texit{\texi{\texi{\texi}\tint{\texit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1995;
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  AAR83079
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  Class I MHC antige
ICAM-3 peptide fra
Anti-hIL12 antibod
Peptide reactive w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ATM gene pro
Breast-cancer asso
Chimaeric peptide
MB#1 library deriv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ATM gene pro
M-ras derived anti
                                                                                                                    6, 2003, 14:57:44; Search time 18.2 Seconds (without alignments) 29.286 Million cell updates/sec
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| Chins2/goddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SinDS2/goddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SinDS2/goddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SinDS2/goddata/geneseq-geneseqp-embl/AA1981.DAT:*
| SinDS2/goddata/geneseqp-embl/AA1981.DAT:*
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| SinDS2/goddata/geneseqg/geneseqp-embl/AA1991.DAT:*
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| SinDS2/goddata/geneseqg/geneseqp-embl/AA1991.DAT:*
| SinDS2/goddata/geneseqg/geneseqp-embl/AA1991.DAT:*
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                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
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AAB40057
AAR50113
AAW36170
AAY0171
AAW30760
AAB87221
AAR97470
                                                                                        protein search, using sw model
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                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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1 DRAT 4
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                        Scoring table:
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IndelB ö

100.0%; Score 20; DB 14; Length 12; 100.0%; Pred. No. 59;

0, Mismatches

Conservative

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Local Similarity 12 AA;

Sequence Query Match Matches

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                                                         AAR83061-R83085, AAR83090-R83080 and AAR83001-Reprehent fragments of clases I major thistocompatibility complex (WHC) antigens. These equances can be used to extend the pariod of acceptance by a recipient of a transplant from an WHC unmarched door. The peptides are administered for a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for ourset restments). The peptides patient the current carrier of the patient for a limited activity of the cyclocate I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intercellular adhesion molecule-3; ICAM-1; ICAM-1; ICAM-2; homology; NK-17, Ig domain; NK-10; domain 4; probe; leukcyte; Jymphocyte; macrophage; neutrophil; inflammation; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inter-cellular adhesion molecule-3 inhibiting granulocyte. Imphocyte and macrophage adhesion - for treating inflammation, AIDS, asfarma, auco-immune thyroiditis, multiple sclerosis, ABDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 16; Length 4; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Disclosure; Page 10; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR30472 standard; peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICAM-3 peptide fragment NK-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US04896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLOO-) CENT BLOOD RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This invention relates to a new human antibody specific for human interlaukinal to the live file. The invention also includes entigen binding portions that bind to IL-12. Requences AR33948-893516 represent human continuous that bind to IL-12. Sequences AR33948-893516 represent human card sequences of the variable respin amino acid sequences are minimal acid sequences. The respect and aria sequences. The variable respin amino acid sequences are given in AA83551-83560 and AA84066-84049. Sequences AA83551-840663 represent anti-IL-12 CMB1 related amino acid sequences are given in AA84064-84067. Primers used in the identification and construction of the antibodies of the invention is a nettralising antibody and has antithematic; antistriction is a nettralising antibody and has antithematic; antistriction are action. The antibodies of the invention is an extralisting antibodies of antistriction are discontinuous entities. The invention are given in the article antibodies of the invention are useful in the treatment of antibodies or antigenthal article antistriction are associated with derinimanal are useful in the treatment of associated and disease. The antibodies of a pharmaceutical composition composition in the mann II-12 classed of human II-12 disorders.
                                                                                                                                                                                  Human, neutralising antibody, interleukin-12; IL-12; antiinflammatory; complementarity determining region. Cont, antihementic, antiarthitic, antiatectoric, neuroprotective, antipsoriatic, antiatementic, antiatementic, antiatementic, antiatementic, antiminionally immunosupersentive; Crohn's disease; mailtipse sciencesis; rhoumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duncan AR;
                                                                                                                                                 Anti-hIL12 antibody light chain CDR3 amino acid sequence SEQ ID 573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yuska M, Paskind M, Banerjee S, Tracey DE, White Labkovsky B, Sakorafas P, Friedrich S, Myles A; tturid A, Warne NW, Widom A, Elvin JG, Duncan P, Carmen S, Smith S, Holtet TL, Du Fou SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 32; Figure 2H; 377pp; English.
                       AAB40057 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0126603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000WO-US07946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaymakcalan Z, Labkovsky
Veldman GM, Venturini A,
Derbyshire EJ, Carmen S,
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BADI ) BASF AG.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roguska M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-638250/61.
                                                                                                                                                                                                                                                                                                                                                               WO200056772-A1
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                        05-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salfeld JG,
                                                              AAB40057;
AAB40057
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The sequences given in AAR30472-73 represent fragments of intercellular adhesion molecule-3 (ICAM-3). Comparisons of these sequences with two mequences from ICAM-1 and ICAM-2 reveals a high degree of homology between NR-17 and sequences alown in the first IG domain of ICAM-2. NR-10 peptide shows weak homology to sequences within domain

ICAM-2. NK

for ICAM-1. These peptide sequences were used to design probes for the isolation of the CDNA encoding ICAM-3 fee also AAA33110-11). CDM-3 is involved in the process by which populations of laukocytes recognise and adhere to callular substrates. ICAM-3 modiates callular interactions with other lymphocytes, macrophages and neutrophils at the site of inflammation and sites of immine responses.

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100.0%; Score 20; DB 18;
100.0%; Pred. No. 96;
iive 0; Mismatches 0;
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                                                                                                                                                                      9503-0508836
                                                                                                                                                  96WO-US07040.
                                                                                                                                                                               95US-0441822
                                                                                                                                                                                         95US-0493092
30-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                          Shiloh Y,
                                                                                                                                                                                                                                                             WPI; 1997-012074/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AA;
                                                                                                          WO9636695-A1
                                                                                                                                                  16-MAY-1996;
                                                                                                                                                                      28-JUL-1995;
                                                                                                                                                                              16-MAY-1995;
                                                                                                                                                                                         21-JUN-1995;
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                                                                                                                              21-NOV-1996
                                                                                                                                                                                                                                          Collins FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY01771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                      carriers
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AC AAY
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide can be used to screen antibodies to select antibodies which are specific for a haemostatic protein and can entibodies which are specific for a haemostatic protein and can between intact and cleaved species of the memostatic protein. The polypeptide corresponds to amino acid residues 320-335 of factor IX. Haemostatic proteins are used in the treatment of haemostatic e.g. thromboembolic diseases. See
                                                                                                                                                                                                                     Polypeptide; peptide; oligopeptide; factor IX; haemostatic protein; antibody; treatment; haemostatic disease; thromboembolic disease.
                                                                                                                                                                                                                                                                                                                                                                                                              Isolating haemostatic proteins free of proteolytic degradation products - using new antibodies which distinguish between intact and cleaved forms of the protein, useful in treatment of haemostatic diseases
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                           Score 20; DB 21; Length 12;
Pred. No. 59;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 15; Length 16;
larity 100.0%; Pred. No. 80;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                 Peptide reactive with antibody specific for factor IX.
                                                                                                                                                                                                                                                                                                                                                    (BLOE-) STICHTING CENT LAB VAN DE BLOEDTRANSFUSI.
                                                                                                                                     AAR50113 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36170 standard; Peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6, Page 25; 32pp; English.
                           100.0%;
ilarity 100.0%;
Conservative 0.
                                                                                                                                                                                                                                                                                                                                  92EP-0202615.
                                                                                                                                                                                                                                                                                                                93WO-NL00174
                                                                                                                                                                                                                                                                                                                                                                       Van Mourik JA:
                                                                                                                                                                            07-OCT-1994 (first entry)
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-101117/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
        12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR50111-R50114.
                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                              26-AUG-1993;
                                                                                                                                                                                                                                                                                                                                  27-AUG-1992;
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13 DRAT 16
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                                                                              4 DRAT 7
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                                                                  1 DRAT
                                                                                                                                                          AAR50113;
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         Sequence
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Matches
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                                                                                                                  RESULT 4
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AMPRISTOR 2 are mouse ANM protein epitoges used to generate polyclonal antihoddes. Antibodies rated against the ANM protein detected a monor-pecifically a High molecular weight of the appected size of 150 km one western lottes of protein lysates darived from fibroblast and lympho- blastoid cell lines. Because of the high frequency of truncation breathing the ANM protein and beta fire truncation breathing the ANM protein and beta fiderified if such proteins in the ANM protein and beta fiderified if such proteins are tabla. Musticossaive genetic and beta fiderified if such that a progressive genetic and proteins and a progressive genetic and a fiderified in the ANM protein are tablated and immune sections. The ANM protein and a progressive genetic and a manufacture of the ANM protein and a highly conserved of crammin region should high product (ANM) 655) has a highly conserved of crammin region should high respect to the catalytic construction properties.
                                                                                                  Ataxia-telangiectasia; A-T; mutated; ATW; 11q22-23; signal transduction; DNA damage; cell cycle control; screening; gene therapy; catalytic; phosphatidylinositol-3 kinase; PI-3; cancer predisposition; carrier; untranslated region; UTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinases A.T mutations affect a variety of tissues and jeed to cancer predignostion. Indentification of A-T carriers by analysis at nucleic acid or protein levels. Allows better supervision and treadment of subjects who are increased risk of developing center and are particularly sensitive to radiation. The transgenic animals and transformed cells are useful as models of the human disease. Also viral vectors expressing the XFM procein can be used in gene therspy of A-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene ATM implicated in ataxia-telangiectasia and related protein - useful in screening methods, partic. for identifying disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
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Mouse ATM gene product epitope 1.
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Gaps

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Indels

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Ataxia-telangiectasia, A-T; mutated, ATW; 11q22-23; signal transduction; DNA damage; cell cycle control; screening; gene therapy; catalytic; phosphatidylinositch-3 kinase; PI-3; cancer predisposition; carrier; unremalared region; UTK.
                                  M-ras, interleukin-9 signaling pathway; pathogenesis; atopic allergy; asthma: leukemia. Lymphoma; Hodgkin's disease; amycosis fungoide.
                                                                                                                                                                                                                                                                                                                                                                                   protein which was used to raise antibodies. W-Ras, a part of the interleukin-9 signaling pehway, is involved in pathogenesis of atopic allorgy, sethma and similar conditions, some leukemias and limphomas and tumors. Agents that downregulate W-Ras are used to treat these conditions, particularly T-cell lymphoma or leukemia; Hodgkin's disease and mycosis fungoides. Westarring levels of M-Ras is used to dispose, or monitor, these conditions (an elevated level being indicative of disease).
                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a peptide derived from M-ras
                                                                                                                                                                                                                                                                Louahed J, Nicolaides N, Renauld J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 20; Length 19; 100.0%; Pred. No. 96; ive 0; Mismatches 0; Indels
             M-ras derived antigenic peptide used to raise antibodies
                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding human or murine M-Ras
                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 17; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW07660 standard; Peptide; 21 AA
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                                                                                                                                                                                 98WO-US19626
                                                                                                                                                                                                          97US-0059509
                                                                                                                                                                                                                                     (MAGA-) MAGAININ PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                Levitt R,
                                                                                                                                                                                                                                                                                          WPI; 1999-244027/20
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es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AA;
                                                                                                                                                                                 18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9636695-A1
                                                                                                Unidentified
                                                                                                                         WO9914242-A2
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16-MAY-1995;
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                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                Grasso L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW07660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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And Worksels, at an entitle date. Antibodies raised against the ATM protein and monoclonal antibodies. Antibodies raised against the ATM protein detected mono-specifically a high molecular weight of the expected size of 350 kbs on Western blots of protein lyastes derived from fibrobiast confidence blastod earl lines because of the high froquency of truncation mutations in the ATM gene, mutated ATM protein can be carried if such proteins are stable. Mutated ATM protein can be carried if such proteins are stable. Mutated ATM protein can be atxis—telangictasia (A-T), a progressive genetic disorder affecting the central narvous and immune systems. The ATM gene, located at case atxis—telangictasia (A-T), a progressive genetic disorder affecting the central inks but damage surveillance to call cycle control. The ATM system that links but damage surveillance to call cycle control. The ATM content content inks but an adverse central randout affect a variety of tissues and lead to cancer predisposition. Indentification of A-T carriers, by analysis at nucleic control newels, allows better supervision and treatment of such subjects who are at increased risk of developing cancer and are controlled to particularly sensitive to radiation. The transgenic animals and the variety of transformed calls are useful as models of the human disease. Also viral received the ATM protein can be used in gene therapy of A-T.
                                                                                                                                                                                                                                                                                                AAW07656-62 are human ATM protein epitopes used to generate polyclonal
                                                                                                                                                                           New gene ATM implicated in ataxia-telangiectasia and related protein - useful in screening methods, partic. for identifying disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; breast cancer; breast cancer associated protein isoform; BPI; breast cancer associated feature; BP; diagnosis; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast-cancer associated protein isoform BPI-20 peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 18;
100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                      (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                          Example 5; Page 104; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB87221 standard, Peptide, 21 AA.
                                                                                                  Tagle DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000; 2000WO-GB03143.
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30-MAR-2000; 2000GB-0007754.
95US-0493092.
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                                                                                                  Shiloh Y,
                                                                                                                                        WPI; 1997-012074/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200113117-A2.
     21-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DRAT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-2001
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                                                                                                  Colline FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB87221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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Cis-element; ligand; highly specific DNA binding domain; HSDB; human; H3-kappa-B; regulatory domain; murine; homologue; LL-6; interleukin; HLA class I gene; HLA-B27; HLA-A; acute phase protein response; syngane; immune response; LL-6; LL-6; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                     New chimaeric peptide(s) including a conformational epitope -
inserted into a peptide having similar native conformation, useful
in vaccines and for determn. of minimal epitope(s) or for mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce openic artibodies (AD), and in vaccines against C. elegans. AD raised against the Can be used for immunoherapy and diagnosis, while the CP can be used diagnostically to detect Ab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present peptide is a chimaentic peptide (PP, contg. a coll contg. a conformation to the conformation of the conformation, enabling the epitope to be presented in an immunologically active conformation.
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
                                                                                                  (HALL-) HAIL INST MEDICAL RES WALTER & ELIZA (UYME ) UNIV MELBOURNE.
   BIOTECH AUSTRALIA PTY LTD.
COMMONWEALTH SCI & IND RES ORG.
COUNCIL QUEENSLAND INST MEDICAL RES.
                                                                                                                                                                                    Saul AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ME#1 library derived peptide, F15-A9b.
                                                                                                                                                                                                                                                                                                                                                                                                           Example 18; Page 45; 99pp; English.
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                                                                                                                                                                                Cooper JA, Good MF, Relf WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US10523
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Matches 4; Conservative
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                                                                                                                                                                                                                                  WPI; 1996-221939/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA;
                                                                             CSL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR91391;
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                                                                                 (CSFC-)
                                                        (com-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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       8X3CCCCCCCCCXXXX44444XXXXXCCCCCCCCCCXXXX44444X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for the screening, diagnosis or correcting to breast cancer (BC), determining the steap or severity of BC, and monitoring the effect of therapy administered to a subject having BC, comprising analysing a sample of body fluid by two diamestical bc, electrophoresis to generate a two-dimensional array of features, comprising a chosen feature whose abundance correlates with BC or predicts the onset or course of BC. The method (I) involves:

Ca analysing a sample of body fluid from the subject by two-dimensional electrophoresis to generate a two-dimensional array of features, correlates a chosen feature whose relative abundance of sach closen feature in the sample with the abundance of that chosen feature correlates the correlates with BC or predicts the onset of BC and (b) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature (BRP) in the test sample. The method is useful for screening, diagnosis or CC prognosis of breast cancer, determining the tage or severity of BC, complete the sample of therapy administered to a subject having BC cc and for identifying a subject a triak of developing at CA MBR310, represents breast cancer associated protein isoform (BRP) cc Pheny and Correct and Corre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                  Screening, diagnosis or prognosis of breast cancer, by analyzing a sample of serum or plasma by two dimensional electrophoresis to detect the presence or level of a breast cancer-associated feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramyosin protein, peptide; unc-15; chimaeric; chimaric;
B-cell; conformational epitope; alpha-helix; CGW4; leucine zipper;
detection; mapping; opsonic antibody; vaccine; immunocherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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note= "unc-15 conformational B-cell epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 22; Length 21; 100.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                         Disclosure; Page 25; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                    WPI; 2001-211252/21.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AA;
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Herath HMAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRAT 4
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AAR97470
ID AAR9
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by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinoms and cancers. AM37196 to AM437204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANY93155-Y93159). The receptor variants reduce proliferation, motility and invasiveness of cancer calls. They can therefore be used to treat or prevent cancer, specifically of the breast or ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; mutant; mutein; osetrogen receptor-alpha; zinc finger; osetrogen receptor-beta; vitanin D receptor; retinic acid receptor; rethings domenon receptor; proliferation; motility; invasiveness cancer; hilytoid hormone receptor; proliferation; motility; invasiveness cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a pharmaceutical composition containing at compare a nuclear said estate to the transcript of the receptor is C region (containing the first incomparison but which lacks the ability to bind osetrogen and/or AP-2 (c finger) but which lacks the ability to bind osetrogen and/or AP-2 (c finger) but which lacks the ability for a spho osetrogen receptor expended and and appropriate the ability of the ability of the ability of a spho osetrogen receptor. Similar variations may be generated in the homologous of other osetrogen-type receptor and a said receptor of thyroid formions receptor (see peptides).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition containing nucleic acid encoding variant estrogen receptor reduces proliferation, motility and invasiveness of cancer cells,
                                                                                                        present invention.

N. B. Pages 66 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                            Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 37;
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                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 22;
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human vitamin D receptor amino acids 18-54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating or preventing cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY93158 standard, peptide; 37 AA.
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442369/38.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast, ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200035955-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                          DRAT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                         28 DRAT
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93158;
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                                                                                                                                                                                                  The sequences given in AAR91378-414 represent peptides that bind to highly specific DRN binding domains (1858)s. * These sequences were record for binding to the H2-kappa-B oligomucleotide which contains the NR-kappa-B binding site, and comprises the sequence given in AAT1359. These peptides may be used in a composition for diagnosis and AAT1359. These peptides may be used that a composition for diagnosis and pene therapy and for modifying the transcription or activity of a gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
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                                                  Synthetic random nucleotide sequences encoding ligand binding domains - identified by screening library of vectors or peptide(s) and useful for gene therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen protein SEQ ID NO:4495.
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 17;
100.0%; Pred. No. 1.46+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11, Page 6295; 9803pp; English.
                                                                                                                                                       Claim 70; Page 196; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG73731 standard; Protein; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colorectal carcinoma
      WPI; 1996-151391/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                          28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH33162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 DRAT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG73731;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
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AAG56794 standard; Protein; 38 AA.
                                                                      18-OCT-2000 (first entry)
             33 DRÁT 36
  1 DRAT 4
                                                          AAG56794;
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                                                                                                                                                                                                                                                                  Novel secreted protein 5' expressed'sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
        Gaps
                                                                                                                                                                                                                                                                                                  AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                 Human, 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; oftomosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
regulation; identification.
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 21; Length 37; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
        Indels
 Pred. No. 1.9e+02;
                                                                                                                                                                                                                                   Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                     Human 5' EST related polypeptide SEQ ID NO:871.
        0; Mismatches
                                                                AAY64710 standard; Protein; 37 AA.
                                                                                                                                                                                                                                                                                     Claim 3, Page 618; 837pp; English.
100.04;
                                                                                                                                                                                       99WO-IB00712.
                                                                                                                                                                                                   98US-0057719.
                                                                                        01-FEB-2000 (first entry)
       , 4; Conservative
                                                                                                                                                                                                                                                WPI; 2000:038446/03.
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Best Local Similarity
Matches 4; Conserv
Best Local Similarity
Matches , 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37 AA;
                                                                                                                                                                                                                                                      N-PSDB; AAZ42324.
                                                                                                                                                                                                                      (GEST ) GENSET.
                                                                                                                                                  Homo sapiens
                                                                                                                                                             WO9953051-A2
                                                                                                                                                                                       09-APR-1999;
                                                                                                                                                                                                    09-APR-1998;
                                                                                                                                                                                                         28-APR-1998;
                               12 DRAT 15
                                                                                                                                                                          21-OCT-1999.
                   1 DRAT 4
                                                                            AAY64710;
                                                   RESULT 13
                                                         AAY64710
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 73090.
                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                        99US-0126785
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                                                                                                                 Arabidopsis thaliana
                                                                                                                                                      EP1033405-A2.
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Gaps

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4; Conservative

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis.
                         Human immune/haematopoietic antigen SEQ ID NO:15450.
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AAM87857 standard; Protein; 38
                                                                      17-JAN-2001; 2001WO-US01354
                                                                                                                                                2000US-022096
2000US-022096
2000US-022451
2000US-02251
2000US-022521
2000US-022521
                07-NOV-2001 (first entry)
                                                                                                                                         2000US-02174
                                                     WO200157182-A2
                                              Homo sapiens
        AAM87857;
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Nuclaic acida encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metaeteass
                                                                                  Ruben SM;
                                                                    (HUMA-) "HUMAN GENOME SCI INC.
                         2000US-0251869.
2000US-0251989.
2000US-0251990.
                                        08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                                                                                 Rosen CA, Barash SC,
                                                                                               WPI; 2001-483426/52.
N-PSDB; AAK60638.
             08-DEC-2000;
                           08-DEC-2000;
                                   08-DEC-2000;
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Claim 11; SEQ ID NO 15450; 3071pp + Sequence Listing; English.

AMK54951 to AAX64702 encode the human immune/haematopoietic antigen (I) and explose admin acid a dequences given in AAM81301 to AAX6491921. (I) have optostatic activity, and can be used in gene therapy and vaccine production. (I) have optostatic activity, and can be used in the prevention, disponsis and treatment of disposes associated with inappropriate (I) expression and treatment of disposes associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mitations or delutions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymuclecides may be used to produce the secreted (I), by inserting the nuclear acids into a host cell and culturing the cell to express the protein. (I) proteins and polymuclecides may be used to produce the secreted (I), by inserting the nuclear edids into a host cell and culturing the cell to express the protein. (I) protein and polymuclecides may be used to produce to addition and cancer manners homeopotetic-relatived cells. AAX64703 cancers and cancer manners have acid by AAX6492 to AAX64950 and AAX64703 concerns from the present invention. AAX64952 to AAX64950 and AAX64700.

38 AA; Sequence

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ö ô Onery Match 100.01; Score 20; DB 22; Length 38; Best Local Similarity 100.04; Pred. NO. 24-02; Americal Matches 4; Conservative 0; Mismatches 0; Indels 1 DRAT 4

Search completed: May 6, 2003, 15:01:02 Job time : 19.2 secs

Q8qzg0 crimean-con Q97hx3 clostridium Q81258 hepatitis c Q8c557 arabidopsis Q8t419 drosophila Q9x43 cenorhabdi

OBrags yersinia pe 091506 calmonalla 09006 caenorhabdi 991040 caenorhabdi 099612 ciona intee 099647 drosophila 09867 criticobium l 09166 coentra rum 091765 thermoplasm

Q81258 Q9C557 Q8T4L9 Q9XW43 Q8ZAG5 Q19006 Q19006 Q19006 Q9GSL2 Q9VSD7

Q98AV5 Q93FT6

. 16

316 316 374 382 457 534 534 607

09MAQ7 **097BB5**

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792 8601 1467 503 1391

Q9M033 QBT4M0 QBT4L8 Q45563 Q8X0V7

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Q9maq7 arabidopsis Q9i951 coturnix co Q45553 bacillus su Q8x0v7 neurospora Q9m033 arabidopsis

Oscuve mus musculu

095P10 09CUV6

O8t4m0 drosophila Q8t4l8 drosophila Q95p10 drosophila

O24284 phoenix red 005562 mycobacteri Q9z5h0 mycobacteri

ALIGNMENTS

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6, 2003, 14:58:45 ; Search time 24.85 Seconds (without alignments 58.041 Willion cell updates/sec
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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sp_bacteria:*
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RESULT

							•		Euteleostomi;	Murinae; Mus.
	361 AA.		1	Last sequence update)	Last annotation update)				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	PRT;		Created)	Last sec	Last and				a, Crania	a; Sciure
	PRELIMINARY;		3Lrel. 17,	3Lrel. 17,	01-JUN-2002 (TrEMBLrel. 21, Last ann	ein.	MOZRIK.	зе).	a; Chordat	a, Rodenti
	PRELIA		01 (Trem	01 (TrEMI	02 (TrEMI	2Rik prot	06100378	lus (Mous	; Metazoa	Eutheria
D9DCH4	Q9DCH4	Q9DCH4;	01-JUN-20	01-JUN-20	01-JUN-20	0610037M02Rik protein.	EIF3SS OR 0610037M02RIK.	Mus musculus (Mouse).	Eukaryota	Mammalia; Eutheri
OPPORT	i i	Ä	텀	텀	텀	DE	공	So	8	8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:* sp_bacteriap:*

sp archeap:*

sp_invertebrate:*
sp_mammal:*

sp_fungi:* sp_human:*

sp_organelle:* sp_phage:*

sp_mpc: *

sp plant:*

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NCBI_TaxID=10090;

SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

KENDING-27081/63; TISSUE-KIDNEY;

KENDING-27081/63; TISSUE-KIDNEY;

KENDING-27081/63; TISSUE-KIDNEY;

KENDING-21085660; PubMed-31127831;

A Alzawa T., Tawaw M., Nibhlar K., Yoohino M., Itoh M., Iehil Y.,

A Alzawa T., Hara A., Pikhlarian Y., Komno H., Adachi J., Pukuda S.,

A Alzawa T., Hara A., Pikhlarian Y., Barlalo W. G., Yamanhaza I.,

A Alzawa T., Marsuda H., Anbhurner M., Barlalo W. G., Canavant T.,

A Radde M., Marsuda H., Anbhurner M., Barlalo W. G., Canavant T.,

A Radde M., Marsuda T., Gasterian T., Boon H., Radlaro H. R., Barke M. Sakai K., Okido T., Furuno M., Anon H., Baldarelli K., Barke M. Sakai K., Okido T., Furuno M., Anon H., Baldarelli K., Barke M. Sakai K.,

A Brownered M. J., Bull D., Hofmann M., Hume D.A., Kamiya M., Lee N.,

A Brownered M. J., Bull D., Hofmann M., Hume D.A., Kamiya M., Lee N.,

A Liyons P., Marchionni L., Marina J., Mazaralli J., Mombaerte P.,

A Liyons P., Marchionni L., Marina J., Mazaralli J., Mombaerte P.,

A Sasaki H., Saro K., Schoebaedt C., Seya T., Shibate Y., Stock K., P.,

A Suruki H., Tayo oka K., Wang K.H., Weitz C., Whitcher C., Wilming L.,

A Whyshwa Boris A., Yoshida K., Haeegawa Y., Kawaji H., Kohtsuki S.,

A Mynshwa Boris A., Yoshida K., Haeegawa Y., Kawaji H., Kohtsuki S.,

"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). EMBL; AK002778; BAB22352.1; MGD; MGI:1913335; Bif385. Hayashizaki Y.;

		,			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	2	OI.	Description
-	39	100.0	361	11	Q9DCH4	Q9dch4 mus muscul
7	36	92.3	315	10	Q9LE16	09le16 arabidopsi
е	36	92.3	315	10	Q93254	093z54 arabidopsi
4	36	92.3	320	10	Q9C928	Q9c928 arabidopsi
S	35	89.7	1344	12	069071	069071 human herp
9	34	87.2	293	10	Q8W4H4	O8w4h4 arabidopsi
7	34	87.2	293	10	004202	004202 arabidopsi
æ	34	87.2	302	۳	043060	043060 schizosacch
đ	34	87.2	377	11	Q921F7	Q921f7 mus muscul
10	33	84.6	381	16	OBUBUO	Q8u8u0 agrobacter
11	33	84.6	510	Ŋ	097251	097251 plasmodium
12	32	82.1	115	s	Q9VY53	09vy53 drosophila
13	32	82.1	332	10	Q9LES7	Q9les7 arabidopsi
14	32	82.1	369	13	093345	093345 gallus gal
15	32	82.1	372	10	005699	005699 nicotiana
16	32	82.1	1639	S	Q9VNF2	Q9vnf2 drosophila

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SECURICE FROM N.A.

KENDING-21046191.

KENDING-210491.

KENDING-21046191.

KENDING-210461
                                                                                     Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Permatophyta, Mamoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida Il: Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                Bowest L. Carning P., Kim C.-J. Koesema B., Meyers M.C., Banh J.,
Bowest L. Carning P., Dale J.M., Goldsmith A.D., Haysshizki Y.,
Bowest J. Jiang P.K., Jones T., Kaniya A., Karlin-Neumann G.,
Rawai J., Jiang P.K., Jones T., Kaniya A., Karlin-Neumann G.,
Rawai J., Lam B., Lee J.M., Liu J., Liu S.X., Mitznia M.,
Nguyen M., Can D., Pham P.K., Quech H.L., Sakurai A.,
Rayen M., Seki M., Suthinkok A., Tanga C.C., Tortuni M., Tamada K.,
Yangamarga T., Yu S., Shinozaki K., Davis R.M., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 10; Length 315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Arabidogaie cDNA clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBBL, AVSS120, AAL25537.1; -
SEQUENCE 315 AA, 36536 MM, 5B1685948965BP08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypotherical 36.7 KDa procein.
         01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
1; Mismatches
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                                      AT3g15460/MJK13 12.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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         SORRERERERES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Makaryota, Viridiplantes, Streptophytta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, endicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicacese, Arabidopsis.
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STRAINECT COLUMBIA,

MAIT X. KOLL S., TOWN C.D., Benito M., Creasy T.H., Haas B., Wu D.,

MAITI X., Moning C.M., Koo H., Fujii C.Y., Utestback T.R.,

MATERISE A. Bommar C.L., White O., Niemman W.C., Fraser C.M.,

"Arabidops in thalian a chromosom TIT Pl. MATERIA promite sequence.",

Brain X. A. S2000 To the Exmel/GenBank/DDBJ databases.

BRAIN ACCA216; ARACA75.1.

SEQUENCE 315 AA; 56356 WM; 2D4327073B9883F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (JaN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                       100.0%; Score 39; DB 11; Length 361; 100.0%; Pred. No. 3.6; ive 0; Mismatches 0; Indels (
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13;
                            Interpro; Improface, Mov34, 2.
Interpro; Improface; P. Tach_extenan.
Pena, PR0139; Mov34, T. Tach_extenan.
PR0139; Mov14, T. Tach_extenan.
Pr0139; Mov34, 2, 1.
Pr020m; P0009425; Mov34, 2, 1.
SEQUENCE 36, A. 38000 MM; 8AA965DCD248E3DE CRC64,
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-CCT-2000 (TrEMBLrel, 15, Last sequence update)
01-OCT-2000 (TrEMBLrel, 15, Last endotation update)
Similarity to unknown protein (MJK13.12 protein)
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091254, 01-DEC-2001 (TERMBLE1. 19, Created)
01-DEC-2001 (TERMBLE1. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 AA
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85.7%; Pred. No. 13;
ive 1; Mismatches
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MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative (
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Conservative
InterPro; IPR000555; Mov34
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DNA Res. 7:131-135(2000).
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 VPHNESE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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Q9LE16;
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Vanada K. Panh J. Banno P., Chang E., Dale J.M., Goldsmith A.D.,
Lee J.M., Tang C., Toriumi M., M. H.C.,
Ramanara Y., No G., Thu S., Boser L., Carnince P., Chen H., Check R.,
Rawalla J., Kim C., Koseene B., Dones T., Kamiya A., Karlinneumann G.,
Rawal J., Kim C., Koseene B., Linn G., Mayers M.C., Miranda M.,
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mukai T., Isegawa Y., Yamanishi K.; midentification of human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema I. Lin J., Meyers W. K., Miranda M., Naruaaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Skim P., Southwick A., Sinozaki K., Davis R.W., Ecker J. R., Theologis A., "Full Length CDNA of gene F14G24.20 (GI:12124616)."

"Pull Length CDNA of gene F14G24.20 (GI:12124616)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.3%; Score 36; DB 10; Length 320;
85.7%; Pred. No. 13;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            "Full Length cDNA of gene F14G24.20 (GI:12324636).";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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Human herpesvirus 7.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Last annotation update)
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MEDLINE=96082321; PubMed=7483822;
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BERL, D32005; BAAGGTO.1, ...
INTERPCO: IRROGO912; Herpes MCP.
Pfam; PF03122; Herpes MCP. 1

PRINTS; PR00235; HSCAPSINING; PR0785

SEQUENCE 1344 AA; 15778 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
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Matches 6; Conserv
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SEQUENCE FROM N.A. STRAIN-C. COLOMBIA. C.A., Brandon R.C., Puhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,
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T29M21.15 OR ATG39990.
Arabidopsis thaliama (Mouse-ear cress).
Spermatophyta; tridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; Rosidae; eurosids II; assaicales; Brassicacese; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOUTUTE FROM N. A. Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Soutubrick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Caturbida C.J., Bower T., Bandya M., Carnicci P., Chen H., Chenk R., Chung M. K., Hayashisaki Y., Ishida J., Kamiya A., Kawai J., Chenk R., Chung M. K., Hayashisaki Y., Ishida J., Kamiya A., Kawai J., Sakure K., Lin J. Liu S. X., Marusaka M., Pham P.X., Sakano H., Kawai J., Sakurai T., Sakurai M., Sakin P., Yamada K., Shinozaki K., Sakurai T., Theologia A. Davis R.M., Shin P., Yamada K., Shinozaki K., Bubli, ANG 2556 AMI 2534 IJ - Bubli, ANG 2556 AMI 2534 IJ - Inceptor IRMO05555 MO94.
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01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UUL-297 (TrEMBLrel. 12, Last annotation update)
01-UUR-202 (TrEMBLrel. 21, Last annotation update)
265 processome regulatory subunit S12 ISOLOG (Putative 265 processome
                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bermatophyta, Magnoliophyta, eudicocyladons; core eudicots; Rosidae,
eurosida II. Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

Balm G.J., Dones T., Banh G., Carninci P., Chen H.,

Palm C.J., Bowser L., Jones T., Banh G., Carninci P., Chen H.,

Relm C.J., Lin J., E. W., Harpshizaki Y., Ishida G., Kanhya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Scher J., Theologis A., Davis R.M.,

Schen J., Theologis A., Davis R.M.,

Schent G. (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeano K., Vornlocher H.-P., Richter-Cook N.J., Merrick W.C.,
Himebuech A.G., Hersteley J.W.B.;
18.11. Chem. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 'AA; 31861 MW; 494C2F9E8F6F47C7 CRC64;
01-WAR-2002 (TrEWHIrel. 20, Last sequence update) - 01-UNW-2002 (TrEWHIrel. 21, Last annotation update) - 265 proteasome regulatory subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Pred. No. 32; 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD005425; Mov34 2; 1.
SMART; SM00232; JAB_MPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPHNES 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteasome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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SEQUENCE FROM N.A.

X WEDLINE=160850, PubMed=11743193,

X WEDLINE=160850, PubMed=11743193,

X WEDLINE=160850, PubMed=11743193,

X WEDLINE=160850, PubMed=11743193,

X OKUTA V.K., Zhou Y., Chen L., Wood G.E., Almaida N.P., Jr., Woo L.,

A Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,

A Chapman P., Clendenning J., Desherage G., Giller W., Graft C.,

X KUYWAIN T., Lavy R., Li M. J., WCClelland E., Palmiseri A.,

X KRAYMONG C., Boune G., Saenphimmacha K., Wu Z., Romero P., Cordon D.,

A Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

A Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Nescet E. W., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,

Nescet E. W., The genome of the natural genetic engineer Agrobacterium tumefaciens
T. Selections
                                                                                                                                                                                Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last an
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                                                                                              Length 302;
                                                                                                                                                                                       IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases,
EMBL, EC012711; AAH12711.1; -.
MRD; MGJ:104683; Fina.
302 AA; 33251 MW; A046E087CF083D84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 AA; 44012 MW; F3D8EF729D1D898C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annocation update)
Similar to farnesyltransferaes, CAAX box, alpha.
                                                                                        Score 34; DB 3;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA.
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                                                                                                                        100.0%; Pred. wc. ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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PROSITE; PS00904; PPTA; UNKNOWN_S.
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                                                                                              87.2%;
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                                                                                                                        Local Similarity 100.
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                 70 VPHNES 75
                                                                                                                                                                                                                                                                               1 VPHNES 6
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SEQUENCE 3
      SEQUENCE
                                                                                              Query Match
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Q8U8U0
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                                                                                  Vamada K. Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D., Alang P.X., Lee J.M., Goldsan C.S., Qatch M.L., Tang C., Toriumi M., Vamanura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Yashanizaki Y., Ichida J., Jones T., Kamiya A., Karlin-Memmann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Marusaka M., Nayusa M. Palm C.J., Sakurai T., Sacou M., Seki M., Shinna P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ekker J.R., Theologis A., Tracy S.E., Shinozaki K., Davis R.W., Full Length, CONN G gener T28021.15/At293998 (G12088652).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variance Annual Control of the Contr
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Grood V., Rajandream M.A., Barrell B.G., Lauber J., Hilbert H.,
Duesterhoeft A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -submitted (PEB-1998) to the EwBL/GenBank/DDBJ ditabases.
-submitted (PEB-1998) to the EwBL/GenBank/DDBJ ditabases.
-submitted (PEB-1998)
-submitted (PEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-UDN-1998 (TrEMBLrel. 06, Created)
01-UDN-1998 (TrEMBLrel. 06, Last sequence update)
01-UDN-1998 (TrEMBLrel. 06, Last sequence update)
Hypochetical 33.3 kDa protein C4C3.07 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom, PD005425; Mov34_2; 1.
SERYT, SM00322; JAB MPN/1.
Initiation factor Proceasome.
SEQUENCE 293 As; 31862 MM; 4742CF7E8F6F47C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enkaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AY091363; AAM14302.1; InterPro; IPR000555; Mov34. InterPro; IPR003640; Mov34_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMBL; AY045824; AAK76498.1; -.
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ProDom; PD005425; Mov34 2; 1.
SMART; SM00232; JAB_MPN; 1.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .fam; PF01398; Mov34; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                  SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VPHNES 6
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043060
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Science 294:2317-2323(2001).

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RAMBARINGS FOR CONTROL OF ALTEREATOR AND ADDRESS OF A RAMBARINGS R.A. GASTER S.E., IN PR. HERAKINS R.A. GASTER F.F., RAMBARINGS S.E., SHidrads S.E., Alabhurner M., Henderson S.N., Ramantides F.G., Scherer S.E., In P., Hebring O., Chan L.X., Ramantides F.G., Change M.C., Malton G.E., Malton G.L., Change M.C., Ragers Y.-H.C., Ragers Y.-H.C., Blazel R.G., Change M., Pfeiffer B.D., Ramar K.H., Doyle C., Baxer E.G., Hell G., Malson C.K., Milton G.L.G., Raxin J.F., Agdasani A., An H.-J., Andrews-Frankoch C., Baldwin D., Raman R.H., Basul A., Baxendale J., Bardwarzoju L., Beaaley E.M., Beeson R.Y., Benney P.V., Benney P., Bardwarz D., Bolchakov S., Raman B.P., Bander J., Bardwarz D., Bolchakov S.M., Rasul A., Bardwar D.A., Buller H., Cadieu E., Chandra I., Andrews D., Botchan M., Bauch B. D., Bordhan D.A., Dalke C. Ozwenport. L.B., Dowles B., Dolcher A., Denge Z., Mays A.D., Dew I., Dietz S.M., Re de Pablos B. Delcher A., Denge Z., Mays A.D., Dew I., Dietz S.M., Re de Pablos B. Delcher A., Denge Z., Mays A.D., Dew I., Dietz S.M., R. Dowle I.E., Downes M., Dugan-Rocha S., Dulkov B.C., Dunn P., Durbin R.J., Doug L.E., Downes M., Dugan-Rocha S., Dulkov B.C., Dunn P., Durbin R.J., Doug L.E., Downes M., Dugan-Rocha S., Dulkov B.C., Dunn P., Durbin R.J., Doug L.E., Downes M., Dugan-Rocha S., Dulkov B.C., Dunn P., R. Harris M.L., Harvey D., Haisan T.J., Harrandez J.R., Houck J., R. Harris M.L., Harvey D., Harris M.C., Ramison J.A., Retchun K.A., Mason K.H., Wei M.-H., Ibegwam C., Rakin M., Malson D.L., Rakin M., Malson D.L., Malson D.L., R. Marchin M., Malson D.L., Malson D.L., R. Malson D.L., Malson D.L., R. Malson D.L., Malson D.L., Malson M., Shuppi M., Nalson D.L., R. Malson D.L., Malson D
                                                                   CG11959 protein.

CG11959 Roc CG1342.

Drosophila melanogaster (Fruit Ely).

Drosophila melanogaster (Fruit Ely).

Praryota / Netazoa / Arthropody / Tracheata / Hexapoda / Insecta /

Praryota / Negorea / Endoperay / Endoperay (Ely)

Praryota / Negorea / Endoperay (Ely)

Praryota / Ely)

Roc / Arthropody (Ely)

Roc / Arthropody (Ely)

Roc / Arthropody (Ely)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13640 MW; CEE29A8C8BF402A8 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annocation update)
                           Last sequence update)
Last annotation update)
      Created)
                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
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(TrEMBLrel. 13, C
(TrEMBLrel. 13, L
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   01-MAY-2000 (TrEMBLrel.
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Matches 5, Conservat
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
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56 VPHNEKD 62
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                       01-MAY-2000
01-MAR-2002
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Q9LES7
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Churcher C.M., Craig A., Davies R.M., Deblin K., Pelkuell T.,
Gentles S., Gwilliam R., Handin N., Harris D., Hoiroyd S., Hornsby T.,
Horrocks P., Jagels K., Jassel B., Kyes S., McLena J., Moule S.,
Murchall K., Wurphy L., Oliver K., Quail M.A., Rajandream M.-A.,
Mutchead S., Kelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodbad K., Webbold C., Barrell B.G.,
The complete nucleotide sequence of chromosome 3 of plasmodium
                                                                                        odedier B. Hinkle G. Gattung S., Hiller N., Blanchard M., Orrollo B., Godden B., Cao Y., Askenazi M., Halling C., Mullin L., Mountel K., Gordon J., Vandin M., Tarrchouk G., Epp M., Liu F., Hountel K., Gordon J., Vandin M., Tarrchouk G., Epp M., Liu F., Flangan C., Crowell C., Gordon J., Lowe C., Scott C., Lappas C., Markelz B., Flangan C., Crowell C., Gurson J., Lowe C., Sear C., Strub G., Gerlo C., Stark G., Gracone sequence of the plant pathogen and biotechnology agent Softwore sequence of the plant pathogen and biotechnology agent Schence 294:332-338(1001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 381;
69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.6%; Score 33; DB 5; Length 510; 83.3%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           381 AA; 39773 MW; 952964CB23ECE3FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MON-1999 (TrEMBLrel. 12, Last smortation update)
PULATIVE DEMOSIONE OF Numan EB1 procesin.
PPCO305W, MALJEZ-30.
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Pred. No. 6
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InterPro; IPR001715; Calponin-like.
InterPro; IPR004953; EB1.
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                                                                          WEDLINB=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                    EMBL; AE009331; AAL44800.1; -. EMBL; AE008283; AAK89427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 400:532-538(1999)
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PROSITE; PS50021; CH;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 381 AA;
                                               SEQUENCE FROM N.A.
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Q9VY53;
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RESULT 12

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09VY53

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WEDLINE-92017650; PubMed-1921969;

From H., Kategiri F., Chua M. -Hi.;

The tobacco transcription activator TGAla binds to a sequence in the compact transcription of a gene encoding a TGAla-related procein.";

MOL. Gen. Genet. 229:181-188 (1991).

-I- SUBCELLULAR LOCATION: WICCLEAR (BY SIMILARITY).

-I- SUBCELLULAR ELOCATION: THE BZIP FAMILY.

TRANSPACY THE WESS. AAA4091.1;

THANSPACY THE SELVENTY.

INTERPRO, IRRO04827; TE_DZIP.
                            Eukaryora, "Virdiplantee; Streptophyra; Embryophyra; Tracheophyra;
Spermetophyta; Megnoliophyta; eudicoryledons; coxo eudicots;
McEridde; euascerida I; Solanales; Solanaceae; McOrians.
NCPI_Tax10497;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 82.1%; Score 32; DB 10; Length 372; Local Similarity 83.3%; Pred. No. 1.1e-02. Holds 65; Conservative 1; Mismatches 0; Indels es 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                             SMART; SM00318; BRLZ; 1.

DRASTTE; PR00035; BLT BASIC; 1.

DRA-binding; Nuclear protein.
SEGUENCE 372 AA; -41991 MM; 56A2730610C9A06E CRC64;
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                                                                                                                                                                                                                                                                                                                               Pfam; PF00170; bZIP; 1.
                                                                                                                                      SEQUENCE FROM N.A.
  ASF-1/G13 protein.
ASF-1/G13.
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Job time: 27.85 secs
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TBMIS 140.

BURAIS (140.

BURAISOES in thaliana (Mouse-ear cress).

BURAISOES, VIXIdiplantes, Streptophyta, Embryophyta, Tracheophyta,

BORMAIOPHYTA, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,

Eurosida II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                   Сарв
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                                                                                                                     SEQUENCE FROM N.A.
Benes V., Murmbach E., Drzonek H., Ansorge W., Mewes H.W., Rudd S.
Lemcke K., Mayor K.F.X., Quetler F., Salanoubat M.;
Submitted (AUG-2000) to the EMBL/Gensank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98259089; PubMeda-9596583;
Kengaku M., Capdevila J., Roditquez-Egteban C., De La Pena J.,
Johnson R. L., Balmonte J.C. I., Tabin C.J.;
"Distinct Why pethways regulating ABR formation and dorsoventral
polarity in the chick limb bud.";
Science 280:1274-1277(199)
BMBL; APG4462; AAC24524.1;
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83.3%; Pred. No. 1.1e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
bamitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL199931; CAC00744.1; -
EMPChetical Protein.
SEQUENCE 332 AA; 37094 WW; F68FA18855BB9EGE CRC64;
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Last annotation update)
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Last annotation update)
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Pfam; PPF00505; HMG box; I.
SMART; SW00399; HMG; 1.
SEQUENCE 369-AA; 40857 WW; BJ
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AC 005699.
DT 01-NOV-1996 (TYEMBLEEL. 01, 0
DT 01-NOV-1996 (TYEMBLEEL. 01, 0
DT 01-UNN-2002 (TYEMBLEEL. 21,
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Best Local*Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      88 LPHNEGE 94
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Q05699
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Gaps

n 5.1.4 p5 4578 Compugen Ltd.
version - 2003
GenCore (c) 1993
Copyright

OM protein - protein search, using sw model

May 6, 2003, 14:58:24; Search time 7 Seconds (without alignments) (without alignments) (41.476 Million cell updates/sec Run on:

US-09-851-422B-8 39 1 VPHNESE 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters:

112892 segs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O00303 homo sapien	P52347 human herpe	P29702 bos taurus	Q61239 mus musculu	Q04631 rattus norv	P49354 homo sapien			•	_	-	Q9pl33 chlamydia m		•		•	P35577 rattus norv	P46096 mus musculu	P21707 rattus norv	P04070 homo sapien	Q17529 caenorhabdi	-	P14291 saccharomyc	O83728 treponema p	P08619 neurospora	Q12766 homo sapien	_		O22608 dunaliella	P49405 caenorhabdi	P37691 escherichia	. P54580 mycobacteri	P53298 saccharomyc
	GI.	IF35 HUMAN	VCAP_HSV7J	PFTA BOVIN	PFTA_MOUSE	PFTA RAT	PFTA HUMAN	YAQA_SCHPO	RL18 HALN1	HM36 CAEEL	CORA_ECOLI	CORA SALTY	Y275_CHLMU	RP1 HUMAN	CEMA CYACA	CORA HABIN	CTNS CABBL	THBG_RAT	SYT1_MOUSE	SYT1 RAT	PRIC HUMAN	YOE4 CAREL	8511_TRYCR	RED1_YEAST	PODK TREPA	NIA NEUCR	Y194 HUMAN	PK3G HUMAN	PYRF XYLFA	RLS DUNSA	RL5 CAEEL	YIBO_ECOLI	Y497 MYCLE	YG43_YEAST
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	Match Length DB	357	1345	340	377	377	379	. 688	182	254	316	316	316	2156	278	315	404	409	421	421	461	523	752	827	901	982	1435	1448	244	271	293	319	355	406
Query	Match	100.0	89.7	87.2	87.2	87.2	87.2	82.1	79.5	79.5	79.5	79.5	79.5	79.5	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	74.4	74.4	74.4	74.4	74.4	74.4
	Score	39	35	34	34	34	34	32	31	31	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30	53	53	29	29	53	53
Result	No.	1	7	m	4	Ŋ	φ	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	53	24	25	56	27	28	53	30	31	32	33

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Gaps 0

Ouery Match 100.04; Score 39; DB 1; Length 357; Best Local Similarity 100.04; Pred. NO. 0.99; Marches 7; Conservative 0; Mismatches 0; Indels Matches 7; Conservative 0; Mismatches 0; Indels

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510 515	524	548	650	707	751 754
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29	29	29	6 6 6	29	29
3.4	36 37	8 6 7 7	644	4.4 2.6	4 4 5

ALIGNMENTS

				punt s (err-s epsiton)			Craniata, vertebrata, Euteleostomi, Catarrhini: Hominidae: Homo					Asano K., Vornlocher HP., Richter-Cook N.J., Merrick W.C.,		initiation factor 3	subunits. Possible roles in RNA binding and macromolecular assembly."					to the EMBL/GenBank/DDBJ databases.	FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF	METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE COMPLEX P170-EIF3.	DIFFERENT SUBUNITS.	SIMILARITY: BELONGS TO THE PSMD7/C6.1A PAMILY.	T,	s and the EMBL outstat	the Buropean Bioinformatics Institute. There are no restrictions on its	use by non-profit institutions as long as its content is in no way modified and this statement is not removed floads by and for commercial	tp://www.isb-sib.ch/annc											ynchesis. 8A70FC6E2BF07737 CRC64;
	AA.	(4	pdate)	200			verte					k N.J.		ryotic	and m					k/DDBJ	AND P	S WITH	AST 10	IA FA	is pro	rmatic	There	ng as	See ht											2BF077
	357	pun e.	ion u	TACCO			nata;					r-Coo)		enka	nding	. (2				enBan	SOSOME	CIATE	AT LE	m2/ce	#	oinfo	ute.	as loi	nent (8	b.ch)										OFCEE
	PRT;	Created) Last semience undate)	annotation update)	at ron							1143;	Richte	1.B.;	humar	RNA DI	52 (195				EMBL/C	OS RIE	ASSC .	ED OF	THE PSN	vright	of Bi	Instit	itions	agreen	isb-si	:		:					:		1, 8A
	ć O	(Rel. 39, Created)	Last	1111			Chordata; Primates;	,			led=934	P.,	ey J.Y	coding	es in	42-270				o the	THE 4	D MRNA	COMPOS	T OT S	is cor	titute	atics	natitu	cense	cense	-	- 11:	90.1;		lov34.	lov34_2	1.	42,	1	564 MW
	STANDARD;	39,	41,	.).		an).				ن	PubM	ther H	Hersh	IAs en	e rol	72:270		:		000) t	IDS TO	IAI AN	.3 IS	BELONG	antro	as Ins	inform	it i	3 a 11	to li	-	03467	AH004	214	555; M	40; M	v34;	Mov3	AB M	37
	SI	(Rel	(Rel.	bunit	į	Hun (Hun	wetazo itheri	9096		A.N. M.	., 01678:	ornio	4.G.,	of cDN	Sesibl	em. 27	Z N WC			NOV-20	N: BIN	YL-TR	EIF.	ITY: E	PROT	e Swie	n Bioi	1-prot	quire	email	-	5; AAL	4 1064	, , , , ,	PROOOS	PR0036	98; Mc	05425	1757	357 AP
RESULT 1 IF35 HUMAN	IF35 HUMAN 000303;	2000	15-JUN-2002 (Rel. 41, Last annotation update)	(eIF3 p47 subunit).	EIF3S5.	Homo sapiens (Human)	Bukaryota; Metazoa; Chordata; Mammalia: Butheria: Primates;	NCBI TaxID=9606;	[1]	TISSIE-I STOR N.A.	MEDLINE=98001678: PubMed=9341143:	Asano K., Vo	Hinnebusch A	"Structure c	subunits. Po	J. Biol. Chem. 272:27042-27052(1997).	SECTIENCE FROM N A	TISSUE=Lung;	Strausberg R	Submitted (NOV-2000)	-i- FUNCTION			-I- SIMILARI	This SWISS-P	between the	the European	use by nor	entitles requires a license agreement (S	or send an e		EMBL; U94855; AAD03467.1;	EMBL; BC000490; AAH00490.1;	MIM. 603914	InterPro; IPR000555; Mov34	InterPro; IPR003640; Mov34_	Pfam; PF01398; Mov34; 1.	ProDom; PD00	SMAKI SMOOT	Initiation ractor; Frotein blosynthesis. SEQUENCE 357 AA; 37564 MW; 8A70FC6E2
RESULT 1 IF35 HUM	5 %	片	ដដ	8 8	NS G	88	36	ĕ	N.	χ α	2 2	æ	RA	RT	E i	2 2	2 0	2	Æ	Z.	ខ	ខ	ပ္ပ	8 5	មួ	ខ	ខ្ល	ពួម	ខ	ပ္ပ	មួ	E E	ž :	5 2	ä	DR	DR	Z Z	ši	. OS

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            Gene 164:1703-174 H 1995).

- FUNCTION: CATALYZEZ THE TRANSFER OF A FARNESYL MOLETY FROM
- PARNESYL PYROPHOSPHATE TO A CYSTEINE AT THE FOURTH POSITION FROM
THE C-TERMINSO OF SEVERAL PROTEINS. THE ALPHA SUBUNIT 1S THOUGHT
TO PARTICIPATE IN A STABLE COMPLEX WITH THE SUBSTRATE FARNESYL-PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U1-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnocation update)
16-OCT-2001 (Rel. 40, Last amnocation update)
16-OCT-2001 (Rel. 40, Last amnocation update)
17-17-17-17-17-17-17-17-17-17-17-17-1
"Structural homology among mammalian and Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and sequencing of the murine farnesyltransferase alpha-encoding ORNA from a cell line which expresses the human papillomavirus type-16 E6 gene."; Gene 164:373-374[1995].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.2%; Score 34; DB 1; Length 340; 100.0%; Pred. No. 8.9; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shirasawa H., Kinoshita T., Shino Y., Mori K., Shimizu K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F884B68203D24E6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 AA
                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS 5 PFTA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Prenyltransferase; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFTA 2.
PFTA 3.
PFTA 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96069614; PubMed=7590362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40494 MW;
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HSSP; Q04631; IFT1.
InterPro; IPR002089; PPTA.
PEam; PF01239; PPTA; 5.
PROSITE; PS00904; PPTA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 VPHNES 236
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REPEAT
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REPEAT
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KOhl N.E., Diehl R.E., Schäber M.D., Rands E., Soderman D.D., He B.,
Moores S.L., Pompliano D.L., Perro-Novick S., Powers S., Thomas K.A.,
Gibbs J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Memalia, Butherla, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovines, Bos
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
- PUNCTION: WALOR PROTEIN OF THE TOGNAMEDAL CAREID.
- SIMILARITY: BELONGS TO THE HERPENTRUBES MAJOR CAPSID PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1345; 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1345 AA, 152931 MW; 93B4D3FF9BF4977E CRC64;
                                                                                                                                                                                                                                                                       Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                              (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.7%; Score 35; DB 100.0%; Pred, No. 24; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                          Alphaherpesvirinae, Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U43400, AAC54720.1; -. InterPro; IPR000912; Herpes MCP. Pfam; PF03122; Herpes_MCP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00235; HSVCAPSIDMCP.
                                                                                                                                                                                                                                   Major capsid protein (MCP).
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=57278;
                                                137 VPHNESE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1181 PHNESE 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
               1 VPMNESE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PHNESE 7
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                                                                                                                                                                              01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY.
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                                                                                                                                           VCAP HSV7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                         VCAP_HSV73
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fearment diplosphate embertate. ";
Blochemistry 37,5812-5618 [1598].
- I FUNCTION: CARLAZES THE TRANSERS OF A FARNESYL MOLETY PROM
FRANKSYL PYROPHOSPHATE TO A CYSTELINE AT THE FOUNTH POSITION PROM
THE C-TEMINUS OF SEVERAL PROTEINS. "THE ALEHA SUBJUIT IS THOUGHT
TO PARTICIAMENT IN A STRAIL CAMPLEM, WITH THE SUBSTRANTE FARNESYL-PP.
THE BETA SOBUNIT BINGS THE PERTING SUBSTRANTS.
- SOBUNIT: HETBOOKER TO THE PROTEIN PROMITTRANSPERAGS ALPHA SUBJUITT.
- SIMILAMENT: BELONGS TO THE PROTEIN PROMITTRANSPERAGS ALPHA SUBJUIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andres D.A., Wilatovich A., Ozeelik T., Wenzlau J.M., Brown M.S., oddetein J.L., Franck U., Coldstein J.L., Franck U., Colds to the two subunits of human CAXX farnesyltransferase and chromosomal mapping of PWTA and PWTB loci and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Last sequence update)
2-UN-2002 (Rel. 41, Last annoration update)
Protein farnesyltransferase alpha subunit (BC 2.5.1..) (CAAX
farnesyltransferase alpha subunit) (RAS proteins prenyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiena (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primetes, Catarthini, Hominidae, Homo.
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44049 MW; DFFFECC1B88BC080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
                                                                                                                                                                                                                  - i - SIMILARITY: CONTAINS 5 PFTA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO-RICH
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MEDLINE=93123261; PubMed=8419339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94102736; PubMed=8276393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR. A1225, A4425.

PDB. 1FT7, 18-WAX-99.

EDB. 1FT7, 18-WOV-99.

EnterPro; 1RR02096, PPTA.

Ffam. PPO1239, PPTA.

TRANSFERSE; PSD9094, PPTA, PROSTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49354; Q9UDC1;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last and
15-UTN-2002 (Rel. 41, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M81225; AAA41833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
150
184
219
258
377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 VPHNES 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPHNES 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences.
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REPEAT
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PFTA HUMAN
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THE BETA SUBUNIT BINDS THE PRPTIDE SUBSTRATE.
SUBUNIT: HETERODIMER OF AM ALPHA AND A BETA SUBUNIT.
SIMILARITY: BELVONS TO THE PROTEIN PRENYLIFANSFERASE ALPHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
mamalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBL TAXID-0116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).

BULLINE-99322062, PubMed-657575;

LONG S. B., Casey P. J., Beese L.S.;

"Cocrystal structure of protein farnesyltransferase complexed with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W.-J., Andres D.A., Goldstein J.L., Brown M.S.;
Cloning and expression of a CONA encoding the alpha subunit of rat
Piltras protein farnesyltransferase.";
Proc. Natl. Acad. Sci. U.S.A. 88:11368-11372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1993 (Rel. 27, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protein farnesyltransferaes alpha subunit (EC 2.5.1.-) (CAAX
farnesyltransferase alpha subunit) (RAS proteins premyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park H.-W., Boduluri S.R., Mocomaw J.F., Casey P.J., Beese L.S.; "Crystal structure of protein farnesyltransferase at 2.25-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.2%; Score 34; DB 1; Length 377; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F3D60B9899F36D66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                  SIMILARITY: CONTAINS 5 PFTA REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
MEDLINE=97218306; Pubmed=9065406;
                                                                                                                                                                                                                                                                                                                                                                                                                              Prenyltransferase, Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Brain;
MEDLINE=92107951; PubMed=1763049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                  EMBL; D49744; BAA08578.1; -.
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                                                                                                                                                                                                                                                                                                                                        MGD; MGI:104683; Fnta.
InterPro; IPR002088; PPTA.
Pfam; PP01239; PPTA; 5.
PROSITE; PS00904; PPTA; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha) (FTase-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 ;
377 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
DOMAIN
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Q04631;
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MEDLINE-11848401; PubMed=11859360;
RA Wood V., Gwallian R., Kajandema M.A., Lyne M., Lyne R., Stewart A., Sgource J., Pearl N., Haylee J., Baker S., Basham D., Bowman S., Ra Frocks K., Erown D., Baker G., Ellilingverth T., Churcher C.M., RA Colline M., Colline W., Carlian M., Davis P., Feltwell T., Fraser A., Colline W., Colline M., Davis P., Feltwell T., Fraser A., Roentles S., Goble A., Hamiln M., Baris D., Hiddagon G., Ra Montanby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Anderse L., Jones M., Leacher S., McDonald S., McLeen J., Aggels K., Anderse L., Onnes M., Leacher S., McDonald S., McLeen J. G., Ray M., Rabinovitch E., Robert S., Mangall K., Murphy L., Niblet D., Odell C., R. A., Mangall K., Murphy L., Niblet D., Odell C., R. R., Robert S., Stavens K., Sharp S., McLee S., Sandders D., Seeger K., Sharp S., R., Huckels S., Murce R., Scharp S., Retwens K., Taylor R. G., Tivey A., Nille S., Wosell D., Hilbert H., R., Roben J., While C., Rockel M., Fritz C., Holzer E., Mosell D., Hilbert H., R., Ber A., Lehater R., Wosell D., Hilbert M., R., Ber A., Lehater R., Wosell D., Hilbert B., R., Challes H., Pritz C., Holzer E., Wosell D., Hilbert S., R., Albert F., Wose S.J., Xiang Z., Huuse M., Caldele H., Pritz C., Holzer E., Wosell D., Milbert S., M., Langer M., Schles M., Pritz C., Molzer E., Wosell D., Milbert S., M., Ander S., Xiang Z., Huuse M., Cadleu E.J., Monthur C., Woore K., Hurer S.M., R., Bager R., R., Chulle J.L., Morotho S., Manchen D., Sterburg S.L., R. Ander E., Wenter S.M., R., Bager R., R., Chulle J.L., Morotho S., Manchen D., Sterburg S.L., R. Ander E., Wenter D., Weller E., Went
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of 8 Bioinformatics and the Brust on estation the burst of the swiss in the swiss by non-profit institutions as long as its connect is in no way modified and this stetement is not removed. Dagge by and for commercial entities allocates allocates allocate swiss stetement is not removed. Bage by and for commercial or send an email to license agreement (see http://www.lsb-sib.ch/announce/or send an email to licenseas absorb.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 82.1%; Score 32; DB 1; Length 688; Best Local Similarity · 83.3%; Pred. NO. 49; Monthes 5; Conservative 1; Mismatches 0; Indels Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 AA; 78178 MW; 3CB29ED7B7A5DEA2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20504483; PubMed=11016950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 268198; CAA92388.1; -.
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Submitted (NWV-2001) to the EMEL/GenBank/DDBJ darabases,
Submitted (NWV-2001) to the EMEL/GenBank/DDBJ darabases,
Submitted (NWV-2001) to the TRANSERS of a RANSASIL WOLTEN FROM
TABLOSTIC PROPERTY OF CYSTEINS AT THE FOURTH POSITION PROM
THE C-TERMING OF SEVERAL POPTERS WITH THE SUBSTRATE FRANSEYL-PP.
THE BETA SUBMITT BINDS THE EMPLY SUBSTRATE FRANSEYL-PP.
SUBMITT: BETARODIMER OF AN ALCHAR AND A SETA SUBMITT:
SUBMITT: BELONGS TO THE PROTEIN PRENVITRANSFERASE ALPHA SUBMITT:
                  Andres D.A., Goldstein J.L., Ho Y.K., Brown M.S.;
"Muteational analysis of alpha subunit of protein farmesyltransferase.
Byidence for a catalytic role.";
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183 PFTA.2.
217 PFTA.3.
251 PFTA.4.
251 PFTA.5.
251 PFTA.5.
164 K--NH. REDUCED ACTIVITY.
44408 MW, B933CBAG7AB32B9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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PEGM; PP01239; PPTA; 5.
PROSITE; PS00304; PPTA; 5.
"""Inferase; Prenyltransferase; Repeat." PRO-RIGH.
                                                                                                                                                        Biol. Chem. 268:1383-1390(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:3782; FNTA.
MIM; 134635; -.
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379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
NCBI_TaxID~4896;
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Q10109;
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MEDLINE-293100795; PubMed-8314774;
MEDLINE-293100795; PubMed-8314774;
Sequence and topology of the CorA magnestim transport systems of
"Sequence and topology of the CorA magnestim transport systems of
Sallononal ary pyphiwurium and Escherichia coli. Identification of a new
class of transport protein.",
J. Biol. Chem. 258:14071-14080(1993).
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STRAIN-KI2 / MG1565,
STRAIN-KI2 / MG1565,
MFDLINE-S236224; PubMed-1379743;
Mandels D.L., Flunket G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84:5 to 86:5 minutes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Becheridhia coli, and
Becheridhia coli Ol37:H7.
Becheridi, Proteobacteria; gamma subdivision; Enterobacteriaceae;
Becheridhia.
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                                                                                      EMBL, 881044; CA862821.1; ALT_SEQ.
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2720CE47A45660A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Magnesium and cobalt transport protein cora.
CORA OR B3816 OR 25333 OR ECS4746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 27;
1; Mismatches
                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AA;
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Unpublished observations (JUN-1999).
Unpublished observations (JUN-1999).

-i- SHGCELLUHAR LOCATION: Nuclear (Probable).

-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE PROPOSED SPLICING
PATTERN HAS BEEN REVISED TO PRODUCE A CORRECT PAIRED-TYPE HOMEOBOX
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pobl.schroder M., Spudich J.L., Jung K.-H., Alam M., Fretas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., Fenome sequence of Halobacterium species NRC-1. ", Fecome sequence of Halobacterium species NRC-1.", Proc. NRL1, Acad. Sci. U.S.A. 97:2176-12181(2000).
                                                                                                                                                                                                                                                                                                         Decogni J. Witmann-Libold B. "Comparative analysis of the protein comparative analysis of the protein comparative analysis of the protein compares of halophilic archaebacteria.";
Surn J. Biochem. 221,777-281(1994).

1. SIMILARITY: BELONGS TO THE LIBP FAMILY OF RIBOSOWAL PROTEINS.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AA; 19680 MW; 1607FD9C5243288B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
30-MX-2000 (Rel. 39, Last sequence update)
30-MX-2000 (Rel. 39, Last annotation update)
Homeobox protein ceh-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 AA
                                                                                                                                                                                                                                             SPECIES=H. Balinarium, STRAIN=DSM 3754;
MEDLINE=94229075; PubMed=8174557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; D33084; D33084.
InterPro; PR001419, Ribosomal L18p.
Pfan; PF00861; Ribosomal L18p; 1.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE005077; AAG19955.1; -.
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Best Local Similarity
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                                                                                                                                                                                                                       SEQUENCE OF 1-23
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Q93352;
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                                                                                                                     SPECIES-S. Cyphimurium, Septime 2314774, Maguire M.E.; Exphimurium, Septime 2330795; Pubmed-8314774, Maguire M.E.; Exphimurium, Smith R.L., Sanke J.L., Sankely M.D., Maguire M.E.; Seguence and Copology of the Cork magnesium transport systems of "Saguence and Copology of the Cork magnesium transport systems of Salmonaila typhimurium and Secterichia coll. Identification of a new Salmonaila typhimurium and Secterichia coll. Identification of a new Jase of transport protein."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stydene; SQ10064, "Cort."
InterPro; PR000523; Cort.
InterPro; PR001648; Cort.
InterPro; PR001648; Cort.
InterPro; PR001648; Cort.
InterPro; PR0016489; Cort.
InterPro; PR0016489; Cort.
InterPro; PR0016499; Cort.
InterPro; PR0016499; Cort.
InterPro; PR001649; Cort.
Interpro; PR016499; Cort.
Interpro; PR01
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-MEDLINE=1156311, PubMed=11258796;
-MEDLINE=1156311, PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Marata T., Tanaka M., Tobe T., Itida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yaunaga T., Kuhara S., Shiba T., Hattori M., Shinaqawa H., Wanaga T., Komplete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res 8.11-22(2001).
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                                    Perna N.T., Plunkett G. 111, Burland V., Mau B., Glasner J.D., Robe D.S., Mayhwa G.P., Brans P.S., Gregor J., Kirkperick H.A., Posta G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Apodeca B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodeca B.J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterobaemorrhagic Escherichia coli 0157:H7."; "Amarue 409:529-5331(201).
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InterPro, IPR004488; CorA transp.
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                                                Pierce E.A., Quinn T., Meehan T., McGee T.L., Berson E.L., Dryja T.P., 
"Mutations in a gene encoding a new oxygen-regulated photoreceptor 
protein cause dominant retinitis pigmentosa.";
Nat. Genet. 22:248-254(1999).
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WHW-*htcp://www.abb.uth.mc-dedl/retnet/",
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BELL, AF143224, AAD44197.1;

DENGL, AF143225, AAD44197.1;

WHELL, AF14322, AAD4419.1;

EMBL, AF141221, AAD2202.1;

EMBL, AF115242, AAD4719.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF152240; AAD46774.1; JOINED. AF152241; AAD46774.1; JOINED.
                             MEDLINE=99318095; PubMed=10391211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٢
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PSS0309, DC, 2.
Vision, Retinitis pigmentosa,
DOMAIN 36 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD46769.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 180100; -.
InterPro; IPR003533; DCX
Pfam; PF03607; DCX; 2.
SMART; SM00537; DCX; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:10263; RP1.
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        687
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EMBL; AF146592
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINBANDH / Niggl
REAd TD., BILLANDER E.C., Shen C., Gill S.R., Heidelberg J.F.,
Read TD., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
Linher C., Hackey E.K., Eveterson J., Utterback T., Berry K., Bass S.,
Linher C., Hackey E.K., Eveterson J., Utterback T., Berry K., Bass S.,
Linher C., Hackey E.K., Rolonay J., McClarty G., Salzberg S.L.,
Edison J., Fraser C.M.,
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.''
Mucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99318096; PubMed=10391212; Bohne S.J., Zuo J., Hide W.A., Sallivan L.S., Heckenlivety J.R., Bohne S.J., Zuo J., Hide W.A., Gal A., Denton M., Inglehearn C.F., Blanton S.H., Daiger S.P.; Mutations in a novel retina-specific gene cause autosomal dominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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30-MAY-2000 (Rel. 39, Late acquence update)
15-JMN-2000 (Rel. 41, Late annotation update)
Oxygen-regulated procein 1 (Retinitis pigmentosa RPI protein)
(Retinitis pigmentosa 1 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 31; DB 1; Length 316; 83.3%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein; Complete proteome.
316 AA; 35475 MW; 0E10E52452CC9A66 CRC64;
                                                                                                                                                                                            Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=83560;
                                            16-0CT'2001 (Rel. 40, Created)
6-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
17-0CT-2001 (Rel. 40, Last annotation update)
17-0CT-2001 (Rel. 40, Last annotation update)
17-0CT-20
   316 AA.
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Nat. Genet. 22:255-259(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 PHNEDE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PHNESE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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Y275 CHLMU
09PL33:
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P56715;
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Magnesium and cobalt transport protein corA
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Job time : 9 secs
                                                                                                      NCBI_TaxID=727;
                     CORA OR HI1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HI1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 PHNES 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PHNES 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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SO THE TRANSPORT OF THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. 801. Evol. 51:382-399(2000).
-!- FUNCTION: May be involved in proton extrusion. Indirectly promotes efficient inorganic carbon uptake into chloroplaste (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Rhodophyta, Bangiophyceae, Porphyridiales, Porphyridiaceae,
Cyanidium.
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gloeckner G., Rosenthal A., Valentin K.-U.; "The structure and gene repertoire of an ancient red algal plastid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Transport; Hydrogen ion transport.
                     Score 31; DB 1; Length 2156;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 278;
                                                               0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88B1050D7836102F CRC64;
                                                                                                                                                                                                                                                                                                     is-ocr-2001 (Rel. 40, Created)
LG-CT-2001 (Rel. 40, Last sequence update)
15-UTW-2002 (Rel. 41, Last semucration update)
CEMA OR VCF10 OR VCF56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                             278 AA
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   envelope (By similarity).
--- SIMILARITY: BELONGS TO THE CEMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RK-1;
MEDLINE=20496959; Pubmed=11040290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32355 MW;
                  79.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR004282; CemA.
Pfam, PF03040; CemA, 1.
                                       Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2771;
                                                                                                                                          803 PHNESK 808
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                                                                                                         2 PHNESE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
15-JUN-2002
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CORA HAEIN
ID CORA HAEIN
AC P44998;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
                                                                                                                                                                                                                                                             CYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                     Query Match
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CEMA_CYACA
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THIS SYSTEM ENTRY IS CORPYIGHT. It is produced through a collaboration between the Swize Institute of Sioinformatics and the EWHI. Outstation the European Bioinformatics Institutions as Institutions on its work of the Course o
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAILSHEE J. KW20. J. ATCC 51907.
STRAILSHEE J. KW20. J. ATCC 51907.
STRAILSHEE J. Adams N.D., White O., Clayton R.A., Kirkness E.P., Kerlsongen A.R., Bult C.J., Tomb D.F., Dougherty B.A., Merrick J.M., Kerlsvage A.R., Bult C.J., Tomb D.F., Goodhery K., Stutten G., Fizhady M., Fielde C.A., Goospary J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Ribe L.D., Fritchhaun J.L., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Fine L.D., Fritchhaun J.L., Phillips C.A., Smith H.O., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Walter J.C., Walter J.A., Small K.V., Fraser C.M., Smith H.O.,
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-!- FUNCTION: PLAYS A ROLLE IN THE TRANSPORT OF MAGNESIUM AND COBALT
IONS (BY SHYLLARITY).
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InterPro; IRR00448; CorA.transp.
Pfan; Pro1144; CorA; 1.
TICRRAMB; TICR00383; corA; 1.
Magnesium; Cobalt; Transmembrane; Transport; Complete proteome.
TRANSEM 257 277 POTENTIAL.
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                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 AA; 36593 MW; DA4EDA284CC68DCC CRC64;
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ive 0; Mismatches
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Haemophilus influenzae.
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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 6, 2003, 14:59:05; Search time 12.25 Seconds (without alignment) 54.934 Million cell updates/sec Run on:

US-09-851-422B-8 39 1 VPHNESE 7 Title: Perfect score: Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 73:* 1: pir1:* 2: pir2:* 3: pir3:* Database :

Pered. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

35	79.5	320 1345 293	000	ID F96570 T41960 H84823	unknown protein, 8 major capsid prote 26S proteasome reg
3 3 4	87.2 87.2	302	000	T40490 A41013 JC4368	probable 26s prote protein farnesyltr protein farnesyltr
4466	87.2 87.2 84.6 84.6		0000	A41625 A47659 A96238 AB3048	protein farnesyltr farnesyl-protein t bioF protein (AF31 8-amino-7-oxonoman
22222	822.1.1	-	00000	T51269 S17715 T37923 D97132	hypothetical prote transcription acti hypothetical prote uncharacterized ph
33333			90000	096691 T19869 T26235 T48753	Nypothetical prote hypothetical prote hypothetical prote hypothetical prote conserved hypothet
31 31	79.5 79.5 79.5 79.5		0000	A47157 B47157 AE0467 AP0918	magnesium transpor magnesium transpor magnesium and coba magnesium and coba
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hypothetical prote hypothetical prote	hypothetical prote hypothetical prote gamma4-crystallin	hypothetical prote lysophospholipase	magnesium transpor hypothetical prote	hypothetical prote hypothetical prote	conserved hypothet thyroxine-binding	synaptotagmin P65 hypothetical prote
G86452 T48162	T45416 T45444 PN0545	AE2360 H69468	A64109 A70638 G64676	G64373 E85082 T14186	G72288 A39567	S09595 F96633
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ALIGNMENTS

RESULT 1 F96570
unknown protein, 80333-82175 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 23-Mar-2001
C. Accession: F96570
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

Ascension: P9650 and Parallainary
Ascension: L300 and Parallainary
Ascension: L3100 and Parallainary
Ascension: L300 and Parallainary
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Ascension: L300 and Parallainary
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Gaps . Length 320; 0; Indels Score 36; DB 2; Pred. No. 6.8; 1; Mismatches Query Match 92.3%; Best Local Similarity 85.7%; Matches 6; Conservative

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222 VPHNESD 228 1 VPHNESE 7 ð a

RESULT 2

major capaid protein - human herpesvirus 7 (strain JI)
(c.Speciaty: human herpesvirus 7 (strain JI)
A;Variety: strain bry
C;Date: 03-bec-1599 #sequence_revision 03-bec-1599 #text_change 21-Jan-2000
C;Accession: T41560
R;Nitholas, J. T41960

submitted to the EMBL Data Library, December 1995

**Description: Determination and analysis of the complete nucleotide sequence of human A.Reference number: Z2022

**Accession: T41960

**Accession: T41960

**Accession: preliminary; translated from GB/EWBL/DDBJ

**Reference: preliminary; translated from GB/EWBL/DDBJ

**Reference: 1-1445 - ANIC->

**Aresidues: 1-1445 - ANIC->

**Arefidues: EMBL:U414400; PIDN:AAC54720.1

1181 PHNESE 1186

q ò

2 PHNESE 7

A; Note: U57 C, Genetics

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protein farmesyltransferase (EC 2.5.1.-) alpha chain - bovine (fragment)
Cipecies: Bos primisedius reuris (cattle)
Cipecies: 16-Oct-1922 #sequence_revision 16-Oct-1992 #text_change. 28-May-1933
CACcession: A41013
R.Kohl, N.E.: Diehl, R.E.; Schaber, M.D.; Rands, E.; Soderman, D.D.; He, B.; Moores, S.
J. Biol, Chem. 26, 18884-1888, 1991
A;Title: Structural homology among mammalian and Saccharomyces cerevisiae isoprenyl-pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 164, 373-374, 1995
Yitle: Clohing and sequencing of the murine farnesyltransferase alpha-encoding cDNA fi
A;Reference number: JC4368, MUID:96069614, PMID:7590362
A;Accession: JC4368
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Alfodecule (1-177 Agre) (1774)
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C;Accession: A41622
C;Accession: A41622
Proc. Natl. Acad. Sci. U.S.A. 86, 11368-11372, 1991
A;Title: Cloning and expression of a cDNA encoding the alpha subunit of rat p21(ras) pro
A;Arference number: A41625; MUID:92107951; PMID:1763049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein farnesyltransferase (BC 2.5.1.-) alpha chain - mouse
NyAlternate names: farnesyltransferase alpha chain
C.Species: Num musculus (house mouse)
C.Jbate: 10-Jan-1996 #sequence_revision 08-Peb-1996 #text_change 20-Jun-2000
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C.Species Rattus norvegicus (Norway rat)
C.Date: 16-0t-1999 #sequence_revision 16-0t-1992 #text_change 05-Nov-1999
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A.Residues: 1-377 -CHES
A.Crose-references: GB:M81225, NID:g206093, PIDN:AAA41833.1; PID:g206099
A.Krose: part of this sequence was confirmed by protein sequencing
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21;
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100.0%; Pred. No. 4..
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A,Residues: 1-340 <KOH>
A,Cross-references: GB:M74083
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Matches 6; Conservative
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Best Local Similarity
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**Nood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A. submitted to the RWBL Data Library, February 1998
A;Reference number: 221910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable 26s proteasome regulatory subunit - fission yeast (Schizosaccharomyces pombe)
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A/Redidutes: 1-30 < MMOD.
A/Crose-references: EMBL:AL021730; PIDN:CAA16829.1; GSPDB:GN00067; SPDB:SPBC4C3.07
A/Experimental source: strain 972h-; cosmid c4C3
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A.Molecule (Type: DNA
A.Residuse; 1-293 -6370>
A.Cross-references: GB:AE002093; NID:92088652; PIDN:AAB95284:1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Arabidopsis thallana (mouse-ear cress)
C.Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                         Length 1345;
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                                                                                                                                     C, Superfamily: varicella-zoster virus major capsid protein
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                                                                                                                                                                                                                                   Score 35; DB 2;
Pred.,No. 53;
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Conservative 0; Mismatches
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A, Experimental source: strain JI
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C; Superfamily: mov-34 protein
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Best Local Similarity
Matches 6, Conserv
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74 VPHNES 79

1 VPHNES 6

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C,Genetics: A,Gene: At2g39990 A,Map position: 2

A, Accession: T40490

75

70 VPHNES

1 VPHNES 6

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Query Match

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C;Accession: AB3048
W. Stand, D. C. Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel, Karp, P.; Komero, P.; Zñang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypotherical protein TBMIS 140 - Arabidopsis thaliana
(Species Arabidopsis thaliana (mouse-ear crees)
C;Detecies Tabidopsis thaliana (mouse-ear crees)
C;Deteci TEJISS9 Haequence_revient 18-Aug-2000 Htext_change 18-Aug-2000
C;Deteci TEJISS9 Haequence_revient 18-Aug-2000
R;Beness W.; Murmbach E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; eubmitted to the Protein Sequence Database, August 2000
A;Reference number: Z53346
A;Accession: TSISS9
                                                                                                                                                                                                                                                                                                                                                              8-amino-7-oxononanoate synthase [imported] - Agrobacterium tumefaciens (strain C58, Dup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A.Reference number: AB2577; PMID:11743193 A.Accession: AB3048 A.Accession: AB3048
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Theathuse: 1-381 AKUR>
A;Cross-references: GS_ARD08689; PIDN:AAL44800.1; PID:g17742441; GSPDB:GN00187
A;Experimental source: strain CS8 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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                                 Length 381;
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                                 Score 33; DB 2;
Pred. No. 35;
0; Mismatches
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71.4%; Pred. No. 49;
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A Residues: 1-332 <BEN>
A, Cross-references: BMBL:AL390921
                                 Query Match 84.6%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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Matches 5; Conserv
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A.; Trile: CDNA cloning of the two subunits of human CAAX farnesyltransferase and chromosed A.Reference number: A47659; WUID:94102736; PMID:8276393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references GELL0413, NID g388755, PIDN:AAA66265.1, PID:g388756
R.Omer C. Krai, A. Diehl, R. E.; Prendergaat, G.C.; Powers, S.; Allen, C.M.; Gibbe Biothemistry 32, all and C.M.; Gibbe Biothemistry 32, all and Companient and Caresyl-protein transferase: cloning, cay Allen Carestorian and Caresyl-protein transferase: cloning, cay Airser cernoe number:
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Science 294, 2223-2328, 201.
Arilla: Geomes Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number; A97355; PMD:11743194
C;Comment: This protein attaches farnesyl residues to a cysteine near the carboxyl termi
C;Keywords: heterodimer; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                farnesyl-protein transferase alpha chain - human
N'Alternate names: CAAX farnesyltransferase alpha chain; FTPase alpha chain; prenyl-prot
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A. Map position. Linear chromosome
C. Superfamily: S-aminolevulinate synthase; glycine C-acetyltransferase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jépecies: Homo saplens (man). Date: 100 Date: 1.0 May-1996 #text_change 21-Jul-2000 Accession: A47659; 848274
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                                                                                           Length 377
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; Note: sequence extracted from NCBI backbone (NCBIP:132814)
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100.0%; Pred, No. 22;
ive 0; Mismatches (
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                                                                                       Query Match 87.2%; Score 34; DB 2; Best Local Similarity 100.0%; Pred. No. 21; Matches 6; Conservative 0; Mismatches
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A:Map position: 8p22-8q11
C;Keywords: heterodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0
Matches 6; Conservative
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A,Molecule type: DNA
A,Residues: 1-381 <KUR>
                                                                                                                                                                                                                                              270 VPHNES 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 VPHINES 275
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                                                                                                                                                                                                            1 VPHNES 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VPHNES 6
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Gaps

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A; Gene: CAC1883

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A; Cross-references: GB: AE004437; NID: 910581178; PIDN: AAG19955.1; GSPDB: GN00138
                                                                                                                                                                                                                                                                                                    568 ribosomal protein L18P [imported] - Halobacterium sp. NRC-1
C;Species Halobacterium sp. NRC-1
C;Dates 02-Pab-2001 Hacquence_Revision 02-Pab-2001 #text_change 16-Pab-2001
Length 1819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 2; Length 183;
Pred. No. 41;
1; Mismatches 0; Indels
Score 32; DB 2; I
Pred. No. 3.1e+02;
                                                     Mismatches
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C,Superfamily: rat ribosomal protein L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3
Matches 5, Conservative
                                                     Conservative
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
                                                                                                                                                             Db 1289 IPHNDSQ 1295
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Job time : 14.25 secs
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                                                                                                       1 VPHINESE 7
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                                                                         C. Accession: 817715 From M. 1. Actaglir, P.; Chua, N. H.

R. From M. 1. Actaglir, P.; Chua, N. H.

Mol. Gen. Genet. 229. 181.181 191

A. Accession: 817715 MID:92017650; PMID:1921969

A. Accession: 817715 MID:92017650; PMID:1921969

A. Accession: 817715 PMID:92017650; PMID:1921969

A. Accession: 181715 PMID:92017650; PMID:1921969

A. Marian prailminary

A. Molacula (Proper mRM)

A. Molacula (Proper mRM)

A. Molacula (Proper mRM)

A. Molacula (Proper mRM)

C. Superfemily: foe/jun DNA-binding domain homology (PID)

Fig. 124 (Domain: Gos/jun DNA-binding domain homology)
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J. Bacteriol, 183, 4823-4836, 2001
A.f.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A.freference number A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.,Accesalon: 13793.
R.Connor, R., Churcher, C. M.; Barrell, B.G.; Rajandream, M.A.; Waleh, S.V.; Wood, V.
submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1.688 «COM»
A;Crogar-ereferences: EMBL:258198; PIDN:CAA92188.1; GSPDB:GN00066; SPDB:SPAC18G6.10
A;Experimental Bources: Errain 972h-; cosmid c18G6
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A.Molecule type: DNA
A.Residues: 1-1813 «KUR»
A.Residues: 1-1813 «KUR»
A.Fores: references: G.B.S.D.S.D.S.D.S.D.S.D.S.D.S.D.S.G.S.D.S.G.S.D.S.G.NO0168
A.Forestimental sources: Clostridium acecoburylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPAC18G6.10 - fission yeast (Schizosaccharomyces pombe)
                          C;Species: Nicotiana sp. (tobacco)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Clostridium acetoburylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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Q2.1%; Score 32; DB 2; Length 372;
Beer Local Similarity 83.1%; Pred. No. 55;
Marches 5; Conservative 1; Mismetches 0; Indels
Marches 5; Conservative 1; Mismetches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 2; Length 688;
Pred. No. 1.1e+02;
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A;Molecule type: DNA
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   ranscription activator TGAla - tobacco
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A;Accession: T37923
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60 PHNETE 65
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Gaps

us-09-851-422b-8.rapb

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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model Run on:

May 6, 2003, 15:01:10 ; Search time 14 Seconds (without alignment) 43.143 Million cell updates/sec US-09-851-422B-8 1 VPHNESE 7 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328255 seqs, 86286685 residues Searched:

328255 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

oggra_6/rodata/1/pubpaa/1090_VBUCAME_pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 755, App	Sequence 722, App	Sequence 4, Appli	Sequence 5, Appli	Sequence 22, Appl	Sequence 6, Appli	Sequence 1, Appli	m	4,	'n	Sequence 6, Appli	Sequence 4, Appli		Sequence 56, Appl	Sequence 56, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 106, App	Sequence 201, App
QI	US-09-809-391-755	US-09-925-302-722	US-08-945-749-4	US-08-945-749-5	US-10-081-051-22	US-08-945-749-6	US-10-182-263-1	US-10-182-263-3	US-10-182-263-4	US-10-182-263-5	US-10-182-263-6	US-09-978-917A-4	US-09-344-882-8	US-09-866-570A-56	US-09-866-572A-56	US-10-182-263-2	US-09-978-917A-2	US-10-029-180-106	US-09-764-898-201
99	6	10	8	8	6	8	6	6	6	6	o	6	6	σ	10	σ	6	σ	°
Tuery Watch Length DB	357	394	316	316	648	315	419	419	419	419	419	419	423	448	448	461	461	491	610
Query Match	100.0	87.2	79.5	79.5	79.5	6.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9
Score	39	34	31	31	31	30	900	30	30	30	30	30	30	30	30	30	30	30	30
Result No.	-	?	3	4	'n	9	7	60	6	10	11	12	13	14	15	16	17	18	19

ò 셤 Sequence 722, Application Us/09925302
Patent No. Us203020044941A1
Patent No. Us203020044941A1
APPLICANT: Rosen et al.
FILE REFERENCE: PAIO4 Wacleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO4 Nucleic Acids, Proteins and Antibodies
CURRENT FAPLICATION NUMBER: US/09/925,302
CURRENT FILIGE DATE: 2001-08-10

Sequence 48731, A Sequence 11657, A Sequence 10, Appl Sequence 10, Appl Sequence 50, Appl Sequence 51, Appl Sequence 24, Appl Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 78, Appl Sequence 195, Appl Sequence 172, Appl Sequence 173, Appl Sequence 173, Appl Sequence 173, Appl Sequence 174, Appl Seque	Sequence 176, App Sequence 2, Appli Sequence 58, Appli Sequence 4164, App
US-09-864-761-48731 US-09-866-570A-10 US-09-866-570A-10 US-09-866-572A-50 US-09-866-572A-50 US-09-886-573A-50 US-09-881-5-19A-31 US-09-881-5-19A-31 US-09-881-5-19A-31 US-09-881-392-16 US-09-881-392-16 US-09-881-392-16 US-09-881-392-16 US-09-881-392-16 US-09-981-392-16 US-09-981-392-16 US-09-981-392-16 US-09-981-392-16 US-09-381-392-16 US-09-381-392-16 US-09-381-392-16 US-09-381-392-101-1372 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543 US-09-738-626-5543	US-09-712-363-176 US-09-827-949-2 US-09-839-884-58 US-09-764-891-4164
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204 204 3002 3002 3002 3004 4433 11134 11173 11173 11237 11237 11237 11237 1124 1167 1167 1167 1167 1167 1167 1167 116	1172 1620 20 45
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ALIGNMENTS

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-809-391-755
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ 1D NOS: 761
SOSTWARE: PatentIn Ver. 2.0
SEQ 1D NO 755
LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 39; DB 9; Length 357; Best Local Similarity 100.0%; Pred. No. 3.9; No. 3.9; Mismatches 7; Conservative 0; Mismatches 0; Indels
                                                                                         APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
                ; Sequence 755, Application US/09809391; Publication No. US20030049618A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 VPHNESE 143
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US-09-925-302-722
JS-09-809-391-755
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EpptICANT, wakan Suman M.
TITLE OF INVESTION: Ebrilche Ruminantium Polypeptides, Antigens, Polynucleotides, e.
TITLE OF INVESTION: Methods of Use
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APPLICANT: GARDNER, Atchard C
APPLICANT: GARDNER, Atchard C
APPLICANT: MACDIARNID, COLIN W
APPLICANT: NACALARNID, COLIN W
APPLICANT: NOW ZEALBAND WISSERT JOHN THE RESERVE OF INVERTION: ALUMINUM RESISTANCE GENE
TILE REPRENCE: 09/5945, 749
CURRENT APPLICATION WUMBER: US/08/945,749
CURRENT PILING DATE: 1999-01-12
GRAENT RILING DATE: 1999-01-12
GRAENT RILING DATE: 1999-01-05-01
                                                                                                                                                                                                              79.5%; Score 31; DB 8; Length 316;
83.3%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 9; Length 648;
Pred. No. 2.8e+02;
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CURRENT APPLICATION NUMBER: US/10/001,051
CURRENT FILING DATE: 2002-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/269,944
PRIOR FILING DATE: 2001-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/10081051
Publication No. US20030044422A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/08945749
; Patent No. US20020138880A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barbet, Anthony F. APPLICANT: Whitmin, Milliam M. APPLICANT: Kamper, Sondra M. APPLICANT: Simble Bigboy H. APPLICANT: Garta, Roman R. APPLICANT: Moreland, Annie L. APPLICANT: Woreland, Annie L. APPLICANT: Woreland, Annie L. APPLICANT: Wongli, Travis C.
                                                                                                                  ; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-08-945-749-5
         EARLIER FILING DATE: 1995-05-01
NUMBER OF SEO ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 648
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Similarity 71.4%;
5; Conservative
                              NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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Matches 5, Conser
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329 MPHNERE 335
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US-08-945-749-6
                                                                          SEQ ID NO 5
                                                                                                                                                                                                              Query Match
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APPLICANT: GARDIER, Richard C
APPLICANT: GARDIER, Richard C
APPLICANT: ANCOLAND COIN W
APPLICANT: ANCARAND UNISERVICES LIMITED
APPLICANT: New Zealand Pescoral Agriculture Research Institut
TITLE OF INVENTION: ALUMINUM RESISTANCE GENE
FILE REPERENCE: 08/945,749
CURRENT PALLICATION WHERE: 19/96-01-12
EARLIER FILICATION WHERE: 1998-01-12
EARLIER FILIGOTON UNHERE: 1996-05-01
EARLIER FILIGO DATE: 1996-05-01
EARLIER FILING DATE: 1996-05-01
WHIGHER FILING DATE: 1996-05-01
WHIGHER FILING DATE: 1996-05-01
WHIGHER FILING DATE: 1996-05-01
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0
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APPLICANT: MACHARAILO, Colin W
APPLICANT: MACHARAILO, Colin W
APPLICANT: ALKIN ROBER J
APPLICANT: ALKIN ALKIN MACHARAILOR
APPLICANT: MACHARAI UNISARVICE LIMITED
APPLICANT: MACHARAI UNISARVICE LIMITED
TITLE DOFINNENTOR: ALMINIUM RESISTANCE GENE
FILE REFERENCE: 08/95, 749
CURRENT PAPLICATION NUMBER: US/08/945, 749
CURRENT FILING DATE: 1998-01-12
EARLIER FRILING DATE: 1998-05-11
EARLIER FRILING DATE: 1998-05-01
EARLIER FRILING DATE: 1998-05-01
                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, Mismatches
PRIOR APPLICATION NUMBER: PCT/USOO/05918
PRIOR PLICATION NUMBER: 5001-03-08
PRIOR PLING DATE: 1999-03:12
PRIOR PLING DATE: 1999-03:12
NUMBER OF SEQ ID NOS: 895
SOFTWARE: PRECENTIN Ver. 2.0
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08945749
Patent No. US20020138880A1
GENERAL INFORMATION:
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Patent No. US20020138880A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            87.2%; (
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83.3%;
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Best Local Similarity 83.35;
--hes 5; Conservative
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-09-925-302-722
                                                                                                                                                                                                                                                                                                                                                                                                       285 VPHNES 290
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227 LPHNES 232
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Gaps
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                                                                                                                                                   Length 419;
                                                                                                                                                                                                                            0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.79+02;
Best Local Similarity 00; Mismatches 0;
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(EDIREAL INFORMATION: US2003002254A1
(EDIREAL INFORMATION: US20030022554A1
(EDIREAL INFORMATION: US20030022554A1
(EDIREAL INFORMATION: USA0ES, BRYAN E
APELICANT: Grintel, Britan W
TITLE OP INVENTION: PROTRIN C DERIVATIVES
FILE REPERRENCE X-1361
(CURRENT PELICATION NUMBER: US/10/182,263
(CURRENT PELICATION NUMBER: GO/18194)
PRIOR APPLICATION NUMBER: GO/18199
PRIOR FILING DATE: 2000-03-14
PRIOR PELICATION NUMBER: GO/18199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SECTION NOS: 12
SUSTWARE: PELECTION NUMBER: GO/18199
NUMBER OF SECTION NOS: 12
SUSTWARE: PELECTION NOS: 12
SUSTWARE: PELECTION NOS: 12
SUSTWARE: PELECTION 3.1
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Publication No US20030022354A1
GENERAL INFORMATION: Bruce E
APPLICANT: Genile, Brune E
APPLICANT: Genile, Brune E
APPLICANT: Genile, Brune H
TITLE OF INVARION: REQUERN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-182-263-4
         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3
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US-10-182-263-5
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2e+02;
hes 0; Indels
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                                                                                                                                                                                                                                                FERTURE:
OCHER INFORMATION: Description of Unknown Organism: Hin
US-08-945-749-6
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Pred. No. 2..7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10182263
Publication No. US20030022354A1
GRERAL INPORMATION:
APPLICANT: Getlitz, Bruce B
APPLICANT: Getlitz, Bruce B
APPLICANT: Grinnell, Brina M
ITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPREMENCE: X-136 202-00-12
CURRENT APPLICATION NUMBER: GO/181946
PRIOR FIRENCE DATE: 2002-00-11
PRIOR FIRENCE DATE: 2000-00-14
NUMBER OF SEQ ID NOS: 12
SOCTAMARE: PREDRIATION NUMBER: GO/189199
NUMBER GO SEG DID NOS: 12
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PABLICATION NO. US20030022334A1
GENERAL INFORMATION NO. US20030022334A1
GENERAL INFORMATION NO. US20030022334A1
GENERAL INFORMATION TOTAL BATUCE RAPLICANT: JOINE, BYAN E
APPLICANT: GITINEL! BATAN E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILLE REFERENCE: K-136.1
CURRENT FILLING DATE: 2002-02-12
PRIOR PLILING DATE: 2002-02-11
PRIOR PLILING DATE: 2002-02-11
PRIOR PLILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN VETSION 3.1
EARLINE PILING DATE: 1995-05-01
NUMBER OF SEQ ID NOS: 16
SEQ ID NO SEQ ID NOS: 16
LENGTH: 315
TYPE: PREF
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/ ORGANISM: Homo sapiens
US-10-182-263-1
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SEQ ID NO 1
LENGTH: 419
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US-10-182-263-1
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APPLICANT: Patland, Beth
APPLICANT: Lutziger, Isabelle
APPLICANT: Wen, Tast-Jung
APPLICANT: Wen, Tast-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/09866572A
Pacent No. US2002013889A1
GENERAL INFORMITON:
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPRENCE: 53679
CURRENT FAPILCATION NUMBER: 09/9/866,572A
CURRENT FILES NATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 423;
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Pred. No. 3e+02;
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                         FILE REYENGE: 2015/3-01
CURRENT APLICATION WUNBER: US/09/344,882
CURRENT FILING DATE: 1999-06-25
PRICE FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 38
SOFFWARE: Patentin Ver: 2.2
SOFFWARE: Patentin Ver: 2.2
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              Behal, Robert
Schnable, Patrick S
Ke, Jinshan
                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Arabidopsis Thaliana
US-09-344-882-8
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                                                                     Johnson, Jerry L
Allred, Carolyn C
Oliver, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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278 IPHNEN 283
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US-09-866-572A-56
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Publication No. 032203002722941
APPLICATION NO. 032203002722941
APPLICANT NORVENTON PROPERIOR C. TITLE OF INVENTION Process C. CORRENCE: COSTONER NORVEN NORVEN CONTRAIN PROCESS C. CORRENT APPLIANCE NORMER: 05/09/978,917A
CURRENT PILING DATE: 2001-10-17
SOUTHARS: PACENTIN VOR: 2.1
SOUTHARS: PACENTIN VOR: 2.1
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100.0%; Pred. No. 2.7e+0;
ative 0; Mismatches
                                                                                                                                Sequence 6, Application US/10182263
Publication No. USZ0030022354A1
GRNERAL INPORMATION:
APPLICANT: GETLICE, BULCE E
APPLICANT: GETLICE, BULCE E
APPLICANT: GETLICE, BULCE E
APPLICANT: GETLICE, BETLOE E
APPLICANT: GETLICE, BETLOE
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPRENEES: X-13a.
CURRENT FILENTION NUMBER: GO/18/19/19
PRIOR FILENTO APPLICATION NUMBER: GO/18/19/9
PRIOR PILION DAME: 2002-02-11
PRIOR FILENT DAME: 2000-03-14
NUMBER OF SEQ 1D NOS: 12
SCOTTWARE: PALENTIN VETSION 3.1
SEQ ID NOS
LENGTH: 319
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Patent No. US2002016217A1

GENERAL INFORMATION:

APPLICANT: Witchel, Basil J

ARPLICANT: Witchel, Eve S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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US-10-182-263-6
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326 VPHNE 330
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US-10-182-263-6
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Sequence:

262574 Total number of hits satisfying chosen parameters:

262574 segs, 29422922 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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ALIGNMENTS

ULT 19-476-755 09-149-476-755 09-140-675, Application US/09149476 atent No. 6420526 atent No. 6420526 ApplicANT: Rosen et al. APPLICANT: Rosen et al. TITLE DE INVENTION: 186 Human Secreted proteins TITLE REPRENCE: 250021 CURRENT APPLICATION NUMBER: US/09/149,476 CURRENT PILICATION NUMBER: PCY/US98/04493	LILING DATE: 1998-03-06 APPLICATION UNMERS: 60/ APPLICATION UNMERS: 60/ APPLICATION UNMERS: 60/ PILLING DATE: 1997-03-07	R FLLING DATE. 1997-03-07 R FLLING DATE. 1997-03-07 R FLLING DATE. 1997-03-07 R FLLING DATE. 1997-05-23 R FLLING DATE. 1997-05-23	APPLICATION NUMBER: 6 PILING DATE: 1997-05- RPILING DATE: 1997-05- RILING DATE: 1997-05- RILING DATE: 1997-05- RILING DATE: 1997-05-
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Sequence 1. Application Us/0842964
Patent No. 195424
Patent No. 19
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100.0%; Pred. No. 30;
tive 0; Mismatches 0; Indels
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM POC COMPALIABLE
OPERATING SYSTEM: PC-D05/MS-D05/ASCII
SOFTWARE: ParentIn Release #1.0, Version #1.30
APPLICATION NAMER: US/08/429,964
FILING DATE: ZY-APR-1995
CLASSIFICATION: 435
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSITALINE:
ATTORNEY/AGENT INFORMATION:
ANAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
ELECTRATION NUMBER: UTSD:432/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/615,715
FILING DAFE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DAFE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
RILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433 CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: UTELECOMMUNICATION INFORMATION TELEPHONE: (512) 418-3000
                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 377 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (713) 789-2679
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Matches 6; Conservative
                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM MEDIUM TYPE: Floppy
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TEXAS
                                                                                                                                                                                                               270 VPHINES 275
                                                                                                                                              1 VPHNES 6
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US-08-429-964-1
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APPLICANT Oddstein, Joseph L.
APPLICANT Reiss, Yuval.
TITLE OF INVENTION: Tetrapeptide-Based Inhibitors of Farnesyl
TITLE OF INVENTION: Transferase
                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 39; DB 4; Length 357; Best Local Similarity 100.0%; Pred. No. 3.1.; Marches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas

COUNTRY: United States of America
ZIP: 77210
ZIP: 77
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PILING DATE: 18 - ARE 1391
CLASSITICATION NUMBER: US 615, 715
FILING DATE: 20 NOV-1990
CLASSITICATION NUMBER: US 615, 715
FILING DATE: 18 - ARE - 1390
CLASSITICATION NUMBER: US 510, 706
FILING DATE: 18 - ARE - 1390
CLASSIFICATION: S10
ATTORNEY AGENT INPORANTION:
NAME: PARKET DAVIG L.
REGISTRATION NUMBER: 21, 165
                                                     ERALIER PILING DARE: 1937-09-05
ERALIER APPLICATION NUMBER: 60/049,610
ERALIER PILING DATE: 1997-06-13
ERALIER PEDILGATION NUMBER: 60/061,060
ERALIER PILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATABLE & Durkee STREET P. D. Box 4433
CITY: Houseon ATABLE Tevan
           EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07863169A
Patent No. 5420245
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TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 377 amind
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 VPHNESE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPHNESE 7
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US-07-863-169A-1
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Gaps

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1 VPHNES 6

87.2%; Score 34; DB 1; Length 377;

Query Match

US-07-935-087-1

RESULT 4 ద

STATE

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Sequence 5. Application US/07853169A
Patent No. 5420345
GRNERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Golderein, Joseph L.
APPLICANT: Reiss V. Vuval
ITILE OF INVENTION: Tetrappide-Based Inhibitors of Parnesyl
ITILE OF INVENTION: Tetrappide-Based Inhibitors of Parnesyl
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: APPLICANT: P. O. 600 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.2%; Score 34; DB 5; Length 377; 100.0%; Pred, No. 30;
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ZIP: 77210
TEALS.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOREY DISK/ASKII
COMPUTER: IN PC COMPUTELE.
COMPUTER: IN PC COMPUTELE.
COMPUTER: MORDERECT 5.1
COMPUTER: NORDERECT 5.1
COMPUTER: NORDERECT 5.1
FILLING DATE: PC COMPUTER
FILLING DATE: PC COMPUTER
FILLING DATE: PC COMPUTER
FILLING DATE: CASTEDIATION DATA:
FILLING DATE: 24 AUGUST 1992 (24.08.92)
MARCHING DATE: 24 AUGUST 1992 (24.08.92)
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                                                       ADDRESSEE: INTHETTON OF THE ADDRESSEE AND ADDRESSEE AND ADDRESSE AND ADDRESSE AND ADDRESSEE AND ADDR
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NAME: PARKER, DAVID L.
REDISTRATION NUMBER: 32,165
REDERRINGF/DOCKER NUMBER: UTPD377PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                   CHARACTERIZATION AND
THE IDENTIFICATION
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amino acid
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TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 VPHINES 275
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PCT-US93-08062-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYEE: FLOPPY DISK
COMPUTER: 1DM PC COMPATIBLE
OPERATING SISTEM: PC-DOG/M9-DOS
SUFFARE: NORDPEREED 5.1 (CONVERTED to CHARRIN APPLICATION DATA:
APPLICATION NUMBER: US/07/935,087
FILING DATE: 19290824
PRIOR*APPLICATION DATA:
APPLICATION NUMBER: 19300824
FILING DATE: 01/16/92
ATTORNEY/ACRIT INFORMATION:
NAME: PARKER: DATA IN-
REGISTRATION NUMBER: 32.165
REPREEDEC/DOCKET NUMBER: 32.165
REPREEDEC/DOCKET NUMBER: 12.165
REPREEDEC/OPERINTON INFORMATION:
TELEBRANE: 512-320-7200.
                                                                                                                                                                                                                                                                                                          APPLICANT: BROWN, MICHAEL S.
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDGEREN, JOSEPH L.
APPLICANT: REISS, YONAL
APPLICANT: REISS, YONAL
APPLICANT: REISS, YONAL
APPLICANT REISS, YONAL
APPLICANT REISS, YONAL
APPLICANT REISS, YONAL
TITLE OF INVESTION: PROTEIN TRANSFERASE
NUMBER OF SEQUENCES: 6
ADDRESSORER: ARROLD, WHITE & DURKEE
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
SEQUENCE CHARACTERISTICS: REISS, "VUML
SEQUENCE CHARACTERISTICS: MASSIERS, JR., JAMES C.
ADDRESSEE: METHODS AND COMPOSITIONS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433 CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9308062
GENERAL INFORMATION:
                                                                                                                                                                                                          Sequence 1, Application US/07935087
Patent No. 6083917
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SEQUENCE CHARACTERSTICS:
LENGTH: 377 amino acide
TYPE: amino acid
FORMATION ACIDE STRANDENESS: alingle
STRANDENESS: alingle
US-07-385-087-1 linear
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                              270 VPHNES 275
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ZIP: 77210
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RESULT 5 PCT-US93-08062-1

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APPLICANT:

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APPLICANT: COLDSTEIN, JÖSSPH L.
APPLICANT: ARISS, YUVAL
APPLICANT: ARISS, YUVAL
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
CORRESPONDENCE ADDRESS:
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30;
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER THE FOOD DISK
COMPUTER THE FOOD DISK
COMPUTER: IMP PC COMPATIBLE
COMPUTER: FOOD DISK
COMPANDED SYSTEM PC DOSK
COMPANDED THE PC DOSK
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COMPANDE
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NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 175D-12/PAR
REPERENCE/DOCKET NUMBER: 175D-12/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-429-964-5
; Sequence 5, Application US/08429964
; Patent No. 5962243
                                                                                            TELECOMORIACATION INFORMATION:
TELECHORIS: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHRANCTERISICS:
LENGTH: 379-amino acids
TYPE: amino acids
                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal US-08-424-268-8
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Best Local Similarity 100
Matches 6; Conservative
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STREET: P.O. BOX 4433
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Fatern No. 582118
GENERAL INCORMATION
APPLICANT: Guer, Charle A
APPLICANT: Guer, Charle A
APPLICANT: Guer, Charle A
APPLICANT: Glab, Nonald E
APPLICANT: Glab, Nonald E
APPLICANT: Glab, Jackson B
COUNTY: United States of America
COMPUTER: RaDABLE FORM:
MSDIWN TYPE: Ploppy disk
COMPUTER: Paver Mac
COM
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30;
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                                                                                                                                                                                                                          PRIOR ADDITIONING DATA:

PRIOR ADDITIONING DATA:

PRINCATE: 19-JAN-19-2-2

CLEAN DATA: 10-JAN-19-2-2

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APPLICATION DATA:
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TATORNEY/AGENT INPORMATION:
NAME: Muthard, David REGISTRATION NUMBER: 35,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.01
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(713) 789-2679
                                                                                                                                          FILING DATE: 03-APR-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 379 amino acids
TYPE: amino acid
STRANBEDNESS: single
TOPOLOGY: linear
US-07-863-169A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 79-0924
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 6; Conservative
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DB 5, Length 379;
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S. SEQUENCE CHARACTERISTICS: GOLDSTBIN, JOSEPH L. SEQUENCE CHARACTERISTICS: REISS, WIVAL. SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES ADDRESSEE: THE IDENTIFICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA

ZIP. 7210

ZIP. 7221

ZIP. 7
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UTFD377PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: THE IDENTIFICATION AND ADDRESSEE: CHARACTERIZATION AND ADDRESSEE: INHIBITION OF ADDRESSEE: FARNESTIRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT. 10442-8
PCT-1059-10442-8
SCHOOLE B. ADDICATION PC/TUS9310442
GENERAL INFORMATION ONE: APPLICANT: Oner, Charles A APPLICANT: Oner, Jackson B APPLICANT: Glibbs, Jackson B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 379 amino acid residues
                                                                                                                                                                                                                                                         ; Sequence 5, Application PC/TUS9308062; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.2.1
100.0%; Pr.
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NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: NOT APPLICABLE INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512-474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FARNESY
NUMBER OF SEQUENCES:
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PCT-US93-08062-5
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                                                                       270 VPHINES 275
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30;
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ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IMP FC COMPATIBLE
APPLICATION NUMBER: US/07/935,087
APPLICATION NUMBER: US/07/922,011
APTIMED APPL FC COMPATION:
NAME: PARKER, DAVID
RECIETATION NUMBER: 13.165
RECIETATION NUMBER: 13.165
RECIETATION NUMBER: 13.165
RECIETATION NUMBER: US/07/822,011
APPLICATION NUMBER: US/07/822,011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS AND COMPOSITIONS FOR THE IDENTIFICATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION OF FARNESYL PROTEIN TRANSFERASE
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TITLE OF INVENTION' CHARACTERIZATION'
TITLE OF INVENTION' CHARACTERIZATION'
TITLE OF INVENTION' RECOTAIN TRANSFERAC
TITLE OF INVENTION' RECOTAIN TRANSFERAC
TITLE OF INVENTION' RECOTAIN TRANSFERAC
CORRESPONDENCE ADDRESS.
ADDRESSEE: AROULD, WHITE & DURKEE
STREET: P.O. BOX 4433
STREET: PLOS TON TRANSFERACE
STREET: ROSTON
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SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acid residues
TYPE amino acid residues
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/07935087
Patent No. 6083917
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
                                                                  TELEX. 19-036.
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 379 and no acids TYRE: and no acid STRANBONESS: aingle TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
(512) 418-3000
(713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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270 VPHNES 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VPHNES 6
TELEPHONE:
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Parent No. 522110 B
GENERAL INFORMATION:
APPLICANT: Omer. Charles A
APPLICANT: Ones. Ackson B
APPLICANT: Other, Ackson B
APPLICANT: Other, Nach Control of APPLICANT: Assay for Inhibitors of Farnesyl-Protein TILE OF INVENTION: Transferase
                                  TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein TITLE OF INVENTION: Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 379;
30;
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                                                                                                                                                                                                                                     STREET P. D. GEAY 2000
CITY: Rahway 2000
CITY: Rahway 2000
COUNTRY: We Joseph States of America
COUNTRY: We Look States of America
COMPUTER RADABLE FORM:
WEDING TEE: REP C. COMPACTION
COMPUTER TEE: REP C. COMPACTION
COMPUTER: REP C. COMPACTION
FILING
FI
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100.0%; Pred. No. 30;
tive 0; Mismatches
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ADDRESSED Merck & Co., Inc.
STREET: Rahwy Co. 20

CITY: Rahwy Co. 20

CITY: Rahwy Co. 20

COUNTRY: United States of America

COUNTRY: United States of America

COUNTRY: Power Pac. 20

COMPUTER READALL FORM: System CONTRY: Power Mac. OPERATING SYSTEM: System 7:5:3

SOFTWARE: MACTORET WAT 5:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION INDEX: 97/968,782
FILING DATE: 100.92
ATTORNEY AGENT INFORMATION:
NAME: Muchard, David A
RESTRANTON INDERE: 5,297
TELEPONEY: (906)594-3993
                                                                                                                  NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSES: Merck & Co., Inc.
STREET: P.O.Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
Kohl, Nancy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.2
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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FRAGMENT TYPE:
PCT-US93-10442-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 VPHNES 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VPHNES 6
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Gaps
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APPLICANT: Diel, Ronald E
APPLICANT: Diel, Ronald E
APPLICANT: Gibbs, Jackson B
APPLICANT: Kohl, Mancy E
APPLICANT: Kohl, Mancy E
APPLICANT: ROH, Mancy E
TITLE OF INVENTION: Assay for Inhibitors of Farnesyl-Protein
TITLE OF INVENTION: Transferase
OWESSPONDENCE ADDRESS: 2
OWESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 819;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REMODES FORM:
WEDING THE PROPRY disk
COMPUTER: PROSONS FORM
SPERMING STSTEM: PO-DOS/MS-DOS
SPERMING: Patentin Release #1.0, Version #1.25
CURRAIN APPLICATION DATA
APPLICATION NOWNEE: PCTY/US93/10442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065-0907
                       US/08/424,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 20, Application PC/TUS9310442; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 107/968,782
ATTORNEY/AGENT INFORMATION:
NAME: Muchard, David A
REASTSTATION NUMBER: 15.297
TELECOMBILICATION : 18959
TELECOMBILICATION : 18959
                                                                               ATTORNEY TANCOMATION:
NAME MARE MEDITARIO DE LA REGISTRATION WITHBERS 12, 297
REFERENCE/COCKET MINERS: 1885/ETELECOMMUTICATION INFORMATION:
TELEFRAN (988) 594-4720
INFORMATION FOR SEQ. ID NO: 20.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.2%; Sc
Best Local Similarity 100.0%; P.
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Merck & Co., Inc. STREET: P.O.Box 2000
                                                                                                                                                                                                                                                                                  LENGTH: 819 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal US-08-424-268-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 819 amino acids
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CURRENT APPLICATION DATA:
                                            4/24/95
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                            FILING DATE: 4/
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 VPHNES 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                          Score 34; DB 5; Length 819;
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                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                             Sequence 89, Application US/08173510B
Patent No. 5747396
GRERAL INFORMATION:
APPLICAT: MATTHEW MOVIE, ET AL.
TILLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon
                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/173,510B
FILING OMER: 23 DEC-193
RACIO APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-193
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-193
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-193
APPLICATION NUMBER: 07/956,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/956,972
FILING DATE: 11-MAY-192
APPLICATION NUMBER: 07/981,721
FIRESTERMING NUMBER: 07/981,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2
ELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (213) 955-0440
                                         N-terminal
                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  protein
NO
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HYPOTHETICAL: NO FRAGMENT TYPE: 1 FRAGMENT TYPE: 1 PCT-US93-10442-20
                                                                                                                                                                                                       710 VPHNES 715
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MOLECULE TYPE:
                                                                                                                                                                      1 VPHNES 6
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US-08-173-510B-88
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2 PHNESE 7

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79.5%; Score 31; DB 1; Length 146; 83.3%; Pred. No. 43;
Sequence 86, Application US/08458218
Patent No. 5/08178
GENERAL INFORMATION:
APPLICATY: MATTHEW MOVIE ET AL.
TILLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF ENQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOW LONG TO THE STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION 135

PLASSIFICATION 10ATA:
APPLICATION ONTA:
APPLICATION NUMBER:
10.400.433

APPLICATION NUMBER:
10.400.433

APPLICATION NUMBER:
11.40V.193

APPLICATION NUMBER:
11.40V.193

APPLICATION NUMBER:
11.40V.193

APPLICATION NUMBER:
11.40V.193

ATTORNEY AGENT INFORMATION:
NUMBER: 9.705

AGENTALION NUMBER: 10.58
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 146 AMINO ACIDS
TYPE: AMINO ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 5, Conservative
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May 6, 2003, 14:57:44 ; Search time 31.85 Seconds (without alignment) 20:286 Million cell updates/ecc
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| SIDS2/gcdata/geneseq_geneseq_emb1/AA1994.DAT: |
| SIDS2/gcdata/geneseq_geneseq_emb1/AA1994.DAT: |
| SIDS2/gcdata/geneseq_geneseq_emb1/AA1995.DAT: |
| SIDS2/gcdata/geneseq_geneseq_emb1/AA2005.DAT: |
| SIDS2/gcdata/geneseq_geneseq_geneseq_emb1/AA2005.DAT: |
| SIDS2/gcdata/geneseq_geneseq_geneseq_geneseq_emb1/AA2005.DAT: |
| SIDS2/gcdata/geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_geneseq_g
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1: /GIDS2/geddara/geneseq/geneseqp-emb1/AA1980_DAT:*

2: /GIDS2/geddara/geneseq/geneseqp-emb1/AA1980_DAT:*

3: /GIDS2/geddara/geneseq/geneseqp-emb1/AA1981_DAT:*

3: /GIDS2/geddara/geneseqfy-emb1/AA1981_DAT:*

5: /GIDS2/geddara/geneseqfy-emb1/AA1981_DAT:*

5: /GIDS2/geddara/geneseqfy-emb1/AA1981_DAT:*

7: /GIDS2/geddara/geneseqfy-emb1/AA1981_DAT:*
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908470 segs, 133250620 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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39
1 VPHNESE 7
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Novel human secret	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Farnesyl-protein t	Arabidopsis thalia	Farnesyltransferas	Rat farnesyl prote	Rat farnesyl trans	Mondo inchange
	9	s	4	9	7	5	6	6	7	
0	AAU3075	4AG0922	AAG0922	AAG0922	AAR14717	4AG3007	ARR4973	AAR7783	AAW0442	APP5715
в Б		21 7	21		12		15	16	17 1	
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* Query Match Length DB	4	54	54	33	-	53	5	37	37	,
Query Match	100.0	۳.	۳.	۳.	.2	.2	7	.2	. 2	0
₩ Ba	100	92	6	6	8	80	8	80	6	ά
Score	£,	36	36	36	34	34	34	34	34	7.5
Result No.	-	7	е	4	S	9	7	80	6	ç

Farnesyltransferas		farnesyl pr	Human farnesyl tra	Protein sequence 2	Human geranylgeran	Lung cancer associ		Novel human diagno		Arabidopsis thalia	Drosophila melanog	Human ORFX protein	H. pylori ORF 11ae	H. pylori ORF 06cp	Canine hookworm Ne	Canine hookworm ne	Drosophila melanog	Protein C peptide	R18 antigen of HTL	Streptococcus suis	Novel human diagno	Protein C heavy ch	ပ	C heavy	Protein C heavy ch	Human protein C ca	Human protein C ca	Ų	Human protein C ca	U	Human protein C ca	잍		Arabidopsis thalia
AAR49734	AAR54830	AAR77841	AAW04431	ABB08436	AAU77150	AAB58384	ABB68133	ABG21522	AAG55461	AAG55460	ABB59281	ABP03959	AAW55657	AAW55295	AAR52989	AAY23597	ABB63601	AAW66095	AAR15744	ABB83175	ABG02914	AAR13048	AAR30723	AAR13047	AAR13724	AAR11838	AAR12192	AAR12193	AAR12194	AAR12195	AAR12196	AAR62654	AAG21970	AAG21969
ŗ	12	19	11	21	21	51	52	22	21	21	22	23	18	18	14	50	22	19	12	23	22	12	14	17	12	12	13	12	12	12	12	15	71	21
379	379	379	379	379	380	394	115	O	332	341	m	7.1	87	0	4	146	534	6	78	233	235	258	261	262	262	262	262	262	262	262	262	263	272	329
		87.2																													٠.		6.9	6.9
3.4	4.	34																				30												30
-	12	13	14	15	1,6	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33	e	35	36	37	38	39	40	41	4.2	43	44	45

ALIGNMENTS

us-09-851-422b-8.rag

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99US-0142154.
99US-0142055.
99US-0142390.
                                                        99US-0134219
99US-0134221
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                                                                                         99US-0134768
                                                                                                               99US-0135124
99US-0135353
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99US-0145085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38-JUL-1999
   The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated that altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells of appressing the proteins are useful for identifying aperate (agonists and antagonists) that bind to them. Cells of the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptides and calls generically engineered to express them are also useful for producing the proteins of the proteins are useful in generic vectination, testing and thereby, and can be used as nutritional supplements. They may be used to the used as nutritional supplements. They may be used to confirm the moder and or nerve tissue growth or regeneration; bone, cartilage, tendon and/or nerve tissue growth or regeneration; confirmed to leaves and in bone, cartilage, tendon and/or stimulation; as anti-inflammatory agents; and in treatment of leavest stimulation; as anti-inflammatory agents; and sequences of novel human secreted proteins of the inventom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                          Query Match 100.0%; Score 39; DB 22; Length 444; Best Local Similarity 100.0%; Pred. No. 6.7; Matches 7; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ 1D NO: 7073.
                                                                                                                                                                                                                                                                                  0; Mismatches
         Claim 20; Page 340; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    AAG09225 standard; Protein; 242 AA
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99US-0123548.
99US-0125788.
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990S-0126785.
990S-0127462.
990S-0128234.
990S-0128714.
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99US-0130891.
99US-0131449.
99US-0132048.
99US-0132484.
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99US-0130449
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                                                                                                                                                                                                                                       Sequence 444 AA;
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Gaps ÷

92.3%; Score 36; DB 21; Length 242; 85.7%; Pred. No. 15; ive 1; Mismatches 0; Indels

6; Conservative

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RESULT 3

AAG09224

Query Match Best Local Similarity Matches 6; Conserv

9915-0160015 9918-0160080 9908-0160080 9908-0160090 9908-0161405 9908-0161405 9918-0161159 9918-0161160 9918-0161160 9918-0161160 9918-0161920

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990S-0159584.
990S-0160741.
990S-0160768.
990S-0160768.
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Wed May
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Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay, genetic mapping; gene expression control; promoter; termination sequence.
                                         Arabidopsis thaliana protein fragment SEQ ID NO: 7072.
AAG09224 standard; Protein; 245 AA
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990S-0126785.
990S-0127462.
990S-0128234.
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                                                                                                                                  2000EP-0301439
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                            17-OCT-2000 (first entry)
                                                                                       Arabidopsis thaliana
                                                                                                                                  25-FEB-2000;
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23-APR-1999;
23-APR-1999;
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29-MAR-1999;
01-APR-1999;
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               AAG09224;
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990S-0132863. 990S-0134256. 990S-0134218. 990S-0134219.

9US-0132487

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9US - 0134370 9US - 013476 9US - 0134941 9US - 0135253 9US - 0135629 9US - 0136021 9US - 0137222 9US - 0137222 9US - 0137528	91076 - 0113884 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	9908. 014.091. 9908. 014.091. 9908. 014.1289. 9908. 014.1289. 9908. 014.2380. 9908. 014.2380. 9908. 014.2380. 9908. 014.2380. 9908. 014.338. 9908. 0144.338. 9908. 0146.388. 9908. 0146.388. 9908. 0146.388. 9908. 0146.388.	9US-01452/
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PR 27-JUL 1999 9918-0145918

PR 26-JUL 1999 9918-0145918

PR 10-ANG 1999 9918-0145918

PR 10-ANG 1999 9918-014518

PR 10-ANG 1999 9918-014518

PR 10-ANG 1999 9918-0147120

PR 11-ANG 1999 9918-015109

PR 1

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99US-0136392.
99US-0137222.
99US-0137528.
99US-0137502.
99US-0137724.
99US-0138699.
99US-0138840.
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990S-0139457.
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990S-0139459.
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990S-0139750.
990S-0139763.
990S-0139817.
990S-0140353.
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99US-0140695.
99US-0140823.
99US-0140991.
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990S-0142390.
990S-0142803.
990S-0142920.
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99US-0144865.
99US-0144085.
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990S-0144334
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990S-0144352
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99US-0139462
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99US-0141842
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99US-0144332
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99US-0145224
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02-AUG-1999;
03-AUG-1999;
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                                                                                                                                           Gaps
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                                                                                                                 Length 245;
                                                                                                                                          Indels
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                                                                                                              core 36; DB 21; red. No. 15; Mismatches 0;
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                                                                                                               Score 36;
Pred. No. 1
                                                                                                                                                                                                                                                    AAG09223 standard; Protein; 315 AA
                        990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                              Query Match 92.3%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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99US-0135629.
99US-0136021.
   9US-0161406
9US-0161359
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                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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                                                                                                                                                                VPHNESE 7
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
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24-MAY-1999;
25-MAY-1999;
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06-APR-1999
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                                                                                                                                                                                                                              RESULT 4
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us-09-851-422b-8.rag

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PT comprises two subunits each having a mol. wt. of 45-50 kD (SDS-PAGB). The tryptic digests of the alpha unit are represented in AAR14712-17, and of the beat unit in AAR14718-2.

The FT enzyme can be used to isolate inhibitors. Such inhibitors can be used to isolate inhibitors. Our hinbitors can be used to block the attachment of farnesyl gps. to ras process states to calls of patients suffering with cancer or pre-encerous states to treat or pallate the cancer.

Per sand AR1571-13, AMR1571-81 and AAQ1441-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsn. comprising purified farnesyl-protein transferase - used to inhibit attachment of farnesyl moiety to RAS protein in
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                / Match Similarity 92.3%; Score 36; DB 21; Length 315; Local Similarity 85.7%; Pred. No. 19; Indels 86 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%; Score 34; DB 12; Length 13; 100.0%; Pred. No. 1.6; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Farnesyl; transferase; FT; inhibitor; p21ras; rat; cancer.
                                                                                                                                                                                                                                                                                                                                                Farnesyl-protein transferase alpha subunit (6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malignant cells and to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG30075 standard, Protein, 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein JL, Reiss Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 8, 87pp, English.
                                                                                                                                                                                                                                      AAR14717 standard; Protein; 13 AA.
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99US-0162142
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                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-339750/46.
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                                                                                                                                            218 VPHNESD 224
                                                                                                           1 VPHNESE 7
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus.
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  29-OCT-1999;
                                                                                                                                                                                                                                                                                                       29-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                         AAR14717;
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                                   Query Match
                                                         Best Loc
Matches
                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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990S-0159637.
990S-0159638.
990S-0159584.
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99US-0161992.
99US-0161993.
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17-OCT-2000 (first entry)

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99US-0144005.
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99US-0144325.
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99US-0144635.
99US-0144884.
99US-0144814.
99US-0145086.
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990S-0145089.
990S-0145192.
990S-0145145.
990S-0145218.
990S-0145276.
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990S-0146388.
990S-0146389.
990S-0147038.
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99US-0147303
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99US-0145918
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99US-0145951
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 Procein identification; signal transduction pathway; metabolic pathway; hybridisation sessy; genetic mapping; gene expression control; promoter; cermination sequence.
     Arabidopsis thaliana protein fragment SEQ ID NO: 35891.
                                                                                   9918-012180
9918-012184
9918-012184
9918-0126764
9918-0126764
9918-012676
9918-012874
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990S-0135353.
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990S-0136021.
990S-0136392.
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99108-013-62-89
99108-013-62-89
99108-013-70-80
99108-013-70-80
99108-013-86-47
99108-013-86-47
99108-013-94-89
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99US-0139463.
99US-0139750.
99US-0139763.
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                                                                        25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                               99US-0134221
99US-0134370
                                                                                                                                                                                                                                           99US-0134768
99US-0134941
                                       Arabidopsis thaliana
                                                  EP1033405-A2
                                                             06-SEP-2000
                                                                                                               29-MAR ~1 999
                                                                                                                                08-APR-1999
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The cDNA (AAQ44397) and amino acid (AAR49739) sequences of rat farnesyltransferase (FT) alpha-subunit were determined. The CDNA may be used to produce recombinant FT, useful for screening potential anticancer agence that prevent expression of palras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New farnesyl transferase inhibitor peptide(s) - based on farnesyl acceptor substrate carboxy terminal sequences, used for the
                                                                                                                                                                                                                                                                                                                 New farnesyl-transferase inhibitors - used for inhibiting attachment of a farnesyl moiety to a p21ras protein in malignant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 15; Length 377; 100.0%; Pred. No. 61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Farnesyl transferase; inhibitor; cancer; ras; p21
                                                                                                                                                                                                                   Reiss Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat farnesyl protein transferase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 116-118; 183pp; English
                                                                                                                                                                                                                   Goldstein JL, Marsters JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR77839 standard; Protein; 377 AA..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-0822011.
90US-0510706.
90US-0615715.
92US-0863169.
                                                                              93WO-US08062
                                                                                                                    92US-0935087
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                                                                                                                                                          (GETH ) GENENTECH INC.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                         WPI; 1994-083105/10.
N-PSDB; AAQ44397.
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N-PSDB; AAQ94410.
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 VPHNES 275
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                                                                              24-AUG-1993;
                                                                                                                    24-AUG-1992;
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20-NOV-1990;
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  WO9404561-A
                                        03-MAR-1994
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                                                                                                                                                                                                                   Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 21; Length 293;
100.0%; Pred. No. 47;
ive 0; Mismatches 0; Indels
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99US-0151303.
99US-0151438.
99US-0151930.
                                                                                                                                                                                                                                                                                                               99US-0157865.
99US-0158029.
99US-0158232.
99US-0158369.
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Matches 6, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VPHNES 79
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Rattus sp

SXXEXEXEXS

Query Match

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AAR49739

377 AA;

Sequence

g 8

RESULT 9 AAW04427

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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (11) in a test sample comparing the expression profile of a gene group in the sample comparising genes selected from (1). The method isc useful for examining the ischaemic condition (e.g. compression ischaemia, occlusive ischaemia or vacopastic ischaemia) by measuring expression profile of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB5002 to ABB57030 to ABB570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              condition related sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse ischaemic condition related protein sequence SEQ ID NO:375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%; Score 34; DB 23; Length 377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
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ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 1003-1004; 2690pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                               ABB57154 standard; Protein; 377 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-034733/04.
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                                                                                                                                                                                                                                                            270 VPHINES 275
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                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW04427 shows the alpha subunit of a farnesyl transferase (FT) enzyme
                                                                                                                                                                                                                                                                             AAR7839 is the alpha subunit of tat farnesyl transferace which is involved in the farnesylation of various callular proteins including the cancer ratated ras proteins. It is used to produce the compete farnesyl transferace molecule which is used to demonstrate the affectiveness of poptide inhibitors capable of inhibiting framesyl transferace. The peptide inhibitors are useful for transity cancers and reservable concers in particular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farnesyl transferase, inhibitor, cancer, tumour, neoplasia, prenyl, ras protein, K-ras B; malignant, detection, identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for farnesyl transferase activity - by determining ability transfer farnesyl moiety to K-Ras B protein, partic. useful for identifying inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.2%; Score 34; DB 16; Length 377; 100.0%; Pred. No. 61; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n B7.2%; Score 34; DB 17; Length 377; Similarity 100.0%; Pred. No. 61; 6; Conservative 0; Mismatches 0; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat farmesyl transferase enzyme alpha subunit.
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                                                                                                                                                                                                                      Example 3; Column 47-50; 55pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW04427 standard; Protein; 377 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-497642/49.
                                                                                                                                                               treatment of cancer
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Rattus rattus WO9634113-A2

30-JUL-1997

AAW04427;

29-APR-1996; 27-APR-1995;

31-OCT-1996

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Gaps

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Indels

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Local Similarity

Matches

377 AA;

Seguence Query Match

N-PSDB; AAT38708

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Gaps
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                                                                                                                                                                                The CDNA encoding the human alpha subunit of FPTsse was isolared from a human placental cDNA library in lambda gill using a bourder FPTsse comba gill using a bourder frame can be used to assess the inhibitory existy of a goo, in the Farsesylation of a procein substrate. The seasy can be used to identify anticancer agence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New farnesyl transferase inhibitor peptide(s) - based on farnesyl acceptor substrate carboxy terminal sequences, used for the
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                Mammalian farnesyl protein transferase prodn. - used in assays for cpds. with inhibitory activity for the identification of
                                                                                                                                                                                                                                                                                                                                 87.2%; Score 34; DB 15; Length 379; 100.0%; Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farnesyl transferase, inhibitor, cancer, ras, p21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human farnesyl protein transferase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. ve.
  Omer CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Column 55-58; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR77841 standard, Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reiss Y;
                                                                                                                                                     Disclosure; Fig 2; 69pp; English
  Kohl NE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-0822011.
90US-0510706.
90US-0615715.
92US-0863169.
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                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
  Gibbs JB,
                                                                                                                                                                                                                                                   The assay can be use
See also AAR54829-32
                                  WPI; 1994-167373/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of cancer
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEXAS
                                                                                                                  anticancer agents
                                                                                                                                                                                                                                                                                                   379 AA;
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                                                N-PSDB; AAQ64887
                                                                                                                                                                                                                                                                                                                                                                                                                                  270 VPHNES 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-1990;
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  Diehl RE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The CDNA (AAQ44395) and amino acid (AAR49734) sequences of human farraes)ltransferase (FT) alpha-atbuir vere determined. The CDNA may be used to produce recombinant FT, useful for screening potential anticancer agents that prevent expression of p21ras.
                                                                                                                                                                                                                                                                                                                                                                                                                                               New farnesyl-transferase inhibitors - used for inhibiting attachment of a farnesyl molety to a p21ras protein in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                Farnesyltransferase; FT, alpha-subunit; p21ras; ras protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 15; Length 379; 100.0%; Pred. No. 62; 1. Nismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farnesyl protein transferase; inhibition; farnesylation.
                                                                                                                                                                                                                                                                                                                                                                 Reiss Y;
                                                                                                                                                                                                                                                                                                                                                                 Marsters JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 26; 183pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR54830 standard; Protein; 379 AA.
                                                                Farnesyltransferase alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha subunit of human FPTase.
                                                                                                                                                                                                                                                 93WO-US08062.
                                                                                                                                                                                                                                                                                 92US-0935087.
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                                (first entry)
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                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-083105/10.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 VPHNES 275
                                                                                                                cancer therapy.
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                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                 24-AUG-1993;
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                                                                                                                                                                                                                                                                               24-AUG-1992;
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                                08-AUG-1994
                                                                                                                                                                                WO9404561-A.
                                                                                                                                                                                                                 03-MAR-1994.
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AAR49734;
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Matches

RESULT 12 AAR54830

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87.2%; Score 34; DB 21; Length 379; ilarity 100.0%; Pred. No. 62; Conservative 0; Mismatches 0; Indels
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es 6; Conserv
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Job time: 33.85 secs
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   ABB08436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAMO4431 shows the alpha subunit of a farnesyl transferase (FT) enzyme derived from a human retinal CONA library. The enzyme was used in a method for identifying FT inhibitors. The method involved screening candidate compounds for the ability to inhibit the transfer of a farnesyl moiety to a K-ras B protein. FT inhibitors act by blocking the attachment of prenyl groups to ras proteins in malignant cells of patients suffering from cancer or precancerous states, and as such are used to treat such conditions.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for farnesyl transferase activity - by determining ability to transfer farnesyl moiety to K-Ras B protein, partic. useful for dentifying inhibitors
                                                                                                                                                                                                                                                             Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl; ras protein; K-ras B; malignant; detection; identification.
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                                            Length 379;
                                                                    Indels
treating cancers and ras-related cancers in particular
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                                                                                                                                                                                                                                         Human farnesyl transferase enzyme alpha subunit.
                                            16;
                                         DB 1
62;
                                          11arity 100.0%; Pred. No. 62; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown MS, Goldstein JL, James GL;
                                                                                                                                                                    AAW04431 standard; Protein; 379 AA.
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                                          Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
                       379 AA;
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                                                                                                     270 VPHNES 275
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Protein sequence 2 relative to the farnesyltransferase of the invention.
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                                                                                                                                                                                                                                                                                                                                                        97KR-0012067.
                                                                                                                                                                                                                                                                                                                                                                                                             97KR-0012067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung HH;
                                                                                                                     Farnesyltransferase; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-020309/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLDS ) LG CHEM LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABA98898
                                                                                                                                                                              Unidentified.
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07-MAY-2002
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